



## SEQUENCE LISTING

<110> Kilian, Andrzej  
Bowtell, David

<120> VERTEBRATE TELOMERASE GENES AND PROTEINS AND USES  
THEREOF

<130> 191106.407C2

<140> 09/502,498

<141> 2000-02-11

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<170> PatentIn Ver. 2.0

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Ala Lys Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg  
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Gly Gly Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro  
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His Ala Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn  
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His Ser Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly  
 180 185 190

Ala Arg Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys  
 195 200 205

Arg Pro Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly  
 210 215 220

Gln Gly Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg  
 225 230 235 240

Gly Phe Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser  
 245 250 255

Leu Glu Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly  
 260 265 270

Arg Gln His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro  
 275 280 285  
 Trp Asp Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu  
 290 295 300  
 Tyr Ser Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser  
 305 310 315 320  
 Ser Leu Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile  
 325 330 335  
 Phe Leu Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro  
 340 345 350  
 Arg Leu Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu  
 355 360 365  
 Leu Gly Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His  
 370 375 380  
 Cys Pro Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg  
 385 390 395 400  
 Glu Lys Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp  
 405 410 415  
 Pro Arg Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln  
 420 425 430  
 Val Tyr Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly  
 435 440 445  
 Leu Trp Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys  
 450 455 460  
 Lys Phe Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu  
 465 470 475 480  
 Thr Trp Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro  
 485 490 495  
 Gly Val Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile  
 500 505 510  
 Leu Ala Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu  
 515 520 525  
 Leu Arg Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg  
 530 535 540  
 Leu Phe Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
 545 550 555 560  
 Ile Arg Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala  
 565 570 575

Glu Val Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg  
 580 585 590  
 Leu Arg Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met  
 595 600 605  
 Asp Tyr Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu  
 610 615 620  
 Arg Leu Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu  
 625 630 635 640  
 Arg Ala Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp  
 645 650 655  
 Asp Ile His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln  
 660 665 670  
 Asp Pro Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala  
 675 680 685  
 Tyr Asp Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile  
 690 695 700  
 Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln  
 705 710 715 720  
 Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser  
 725 730 735  
 Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu  
 740 745 750  
 Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser  
 755 760 765  
 Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe  
 770 775 780  
 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys  
 785 790 795 800  
 Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu  
 805 810 815  
 Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp  
 820 825 830  
 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His  
 835 840 845  
 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro  
 850 855 860  
 Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro  
 865 870 875 880

Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala  
 885 890 895  
 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu  
 900 905 910  
 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala  
 915 920 925  
 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg  
 930 935 940  
 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp  
 945 950 955 960  
 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile  
 965 970 975  
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro  
 980 985 990  
 Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile  
 995 1000 1005  
 Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala  
 1010 1015 1020  
 Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu  
 1025 1030 1035 1040  
 Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg  
 1045 1050 1055  
 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln  
 1060 1065 1070  
 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu  
 1075 1080 1085  
 Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 1090 1095 1100

<210> 5  
 <211> 884  
 <212> PRT  
 <213> Homo sapiens

<400> 5  
 Met Lys Ile Leu Phe Glu Phe Ile Gln Asp Lys Leu Asp Ile Asp Leu  
 1 5 10 15

Gln Thr Asn Ser Thr Tyr Lys Glu Asn Leu Lys Cys Gly His Phe Asn

20 25 30  
 Gly Leu Asp Glu Ile Leu Thr Thr Cys Phe Ala Leu Pro Asn Ser Arg  
 35 40 45  
 Lys Ile Ala Leu Pro Cys Leu Pro Gly Asp Leu Ser His Lys Ala Val  
 50 55 60  
 Ile Asp His Cys Ile Ile Tyr Leu Leu Thr Gly Glu Leu Tyr Asn Asn  
 65 70 75 80  
 Val Leu Thr Phe Gly Tyr Lys Ile Ala Arg Asn Glu Asp Val Asn Asn  
 85 90 95  
 Ser Leu Phe Cys His Ser Ala Asn Val Asn Val Thr Leu Leu Lys Gly  
 100 105 110  
 Ala Ala Trp Lys Met Phe His Ser Leu Val Gly Thr Tyr Ala Phe Val  
 115 120 125  
 Asp Leu Leu Ile Asn Tyr Thr Val Ile Gln Phe Asn Gly Gln Phe Phe  
 130 135 140  
 Thr Gln Ile Val Gly Asn Arg Cys Asn Glu Pro His Leu Pro Pro Lys  
 145 150 155 160  
 Trp Val Gln Arg Ser Ser Ser Ser Ser Ala Thr Ala Ala Gln Ile Lys  
 165 170 175  
 Gln Leu Thr Glu Pro Val Thr Asn Lys Gln Phe Leu His Lys Leu Asn  
 180 185 190  
 Ile Asn Ser Ser Ser Phe Phe Pro Tyr Ser Lys Ile Leu Pro Ser Ser  
 195 200 205  
 Ser Ser Ile Lys Lys Leu Thr Asp Leu Arg Glu Ala Ile Phe Pro Thr  
 210 215 220  
 Asn Leu Val Lys Ile Pro Gln Arg Leu Lys Val Arg Ile Asn Leu Thr  
 225 230 235 240  
 Leu Gln Lys Leu Leu Lys Arg His Lys Arg Leu Asn Tyr Val Ser Ile  
 245 250 255  
 Leu Asn Ser Ile Cys Pro Pro Leu Glu Gly Thr Val Leu Asp Leu Ser  
 260 265 270  
 His Leu Ser Arg Gln Ser Pro Lys Glu Arg Val Leu Lys Phe Ile Ile  
 275 280 285  
 Val Ile Leu Gln Lys Leu Leu Pro Gln Glu Met Phe Gly Ser Lys Lys  
 290 295 300  
 Asn Lys Gly Lys Ile Ile Lys Asn Leu Asn Leu Leu Ser Leu Pro  
 305 310 315 320  
 Leu Asn Gly Tyr Leu Pro Phe Asp Ser Leu Leu Lys Lys Leu Arg Leu

325                      330                      335  
 Lys Asp Phe Arg Trp Leu Phe Ile Ser Asp Ile Trp Phe Thr Lys His  
                                  340                                   345                                   350  
 Asn Phe Glu Asn Leu Asn Gln Leu Ala Ile Cys Phe Ile Ser Trp Leu  
                                  355                                   360                                   365  
 Phe Arg Gln Leu Ile Pro Lys Ile Ile Gln Thr Phe Phe Tyr Cys Thr  
                                  370                                   375                                   380  
 Glu Ile Ser Ser Thr Val Thr Ile Val Tyr Phe Arg His Asp Thr Trp  
 385                                   390                                   395                                   400  
 Asn Lys Leu Ile Thr Pro Phe Ile Val Glu Tyr Phe Lys Thr Tyr Leu  
                                  405                                   410                                   415  
 Val Glu Asn Asn Val Cys Arg Asn His Asn Ser Tyr Thr Leu Ser Asn  
                                  420                                   425                                   430  
 Phe Asn His Ser Lys Met Arg Ile Ile Pro Lys Lys Ser Asn Asn Glu  
                                  435                                   440                                   445  
 Phe Arg Ile Ile Ala Ile Pro Cys Arg Gly Ala Asp Glu Glu Glu Phe  
                                  450                                   455                                   460  
 Thr Ile Tyr Lys Glu Asn His Lys Asn Ala Ile Gln Pro Thr Gln Lys  
 465                                   470                                   475                                   480  
 Ile Leu Glu Tyr Leu Arg Asn Lys Arg Pro Thr Ser Phe Thr Lys Ile  
                                  485                                   490                                   495  
 Tyr Ser Pro Thr Gln Ile Ala Asp Arg Ile Lys Glu Phe Lys Gln Arg  
                                  500                                   505                                   510  
 Leu Leu Lys Lys Phe Asn Asn Val Leu Pro Glu Leu Tyr Phe Met Lys  
                                  515                                   520                                   525  
 Phe Asp Val Lys Ser Cys Tyr Asp Ser Ile Pro Arg Met Glu Cys Met  
                                  530                                   535                                   540  
 Arg Ile Leu Lys Asp Ala Leu Lys Asn Glu Asn Gly Phe Phe Val Arg  
 545                                   550                                   555                                   560  
 Ser Gln Tyr Phe Phe Asn Thr Asn Thr Gly Val Leu Lys Leu Phe Asn  
                                  565                                   570                                   575  
 Val Val Asn Ala Ser Arg Val Pro Lys Pro Tyr Glu Leu Tyr Ile Asp  
                                  580                                   585                                   590  
 Asn Val Arg Thr Val His Leu Ser Asn Gln Asp Val Ile Asn Val Val  
                                  595                                   600                                   605  
 Glu Met Glu Ile Phe Lys Thr Ala Leu Trp Val Glu Asp Lys Cys Tyr  
                                  610                                   615                                   620  
 Ile Arg Glu Asp Gly Leu Phe Gln Gly Ser Ser Leu Ser Ala Pro Ile

625                      630                      635                      640  
 Val Asp Leu Val Tyr Asp Asp Leu Leu Glu Phe Tyr Ser Glu Phe Lys  
                                  645                      650                      655  
 Ala Ser Pro Ser Gln Asp Thr Leu Ile Leu Lys Leu Ala Asp Asp Phe  
                                  660                      665                      670  
 Leu Ile Ile Ser Thr Asp Gln Gln Gln Val Ile Asn Ile Lys Lys Leu  
                                  675                      680                      685  
 Ala Met Gly Gly Phe Gln Lys Tyr Asn Ala Lys Ala Asn Arg Asp Lys  
                                  690                      695                      700  
 Ile Leu Ala Val Ser Ser Gln Ser Asp Asp Thr Val Ile Gln Phe  
 705                                   710                      715                      720  
 Cys Ala Met His Ile Phe Val Lys Glu Leu Glu Val Trp Lys His Ser  
                                  725                      730                      735  
 Ser Thr Met Asn Asn Phe His Ile Arg Ser Lys Ser Ser Lys Gly Ile  
                                  740                      745                      750  
 Phe Arg Ser Leu Ile Ala Leu Phe Asn Thr Arg Ile Ser Tyr Lys Thr  
                                  755                      760                      765  
 Ile Asp Thr Asn Leu Asn Ser Thr Asn Thr Val Leu Met Gln Ile Asp  
                                  770                      775                      780  
 His Val Val Lys Asn Ile Ser Glu Cys Tyr Lys Ser Ala Phe Lys Asp  
 785                                   790                      795                      800  
 Leu Ser Ile Asn Val Thr Gln Asn Met Gln Phe His Ser Phe Leu Gln  
                                  805                      810                      815  
 Arg Ile Ile Glu Met Thr Val Ser Gly Cys Pro Ile Thr Lys Cys Asp  
                                  820                      825                      830  
 Pro Leu Ile Glu Tyr Glu Val Arg Phe Thr Ile Leu Asn Gly Phe Leu  
                                  835                      840                      845  
 Glu Ser Leu Ser Ser Asn Thr Ser Lys Phe Lys Asp Asn Ile Ile Leu  
                                  850                      855                      860  
 Leu Arg Lys Glu Ile Gln His Leu Gln Ala Tyr Ile Tyr Ile Tyr Ile  
 865                                   870                      875                      880  
 His Ile Val Asn

<210> 6  
 <211> 13  
 <212> DNA  
 <213> Homo sapiens  
 <220>

<221> intron  
 <222> (8)..(13)  
 <223> First six bases of Y intron

<400> 6  
 ccaggtgggc ctc 13

<210> 7  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last seven bases of intron Y

<400> 7  
 gcaggtgtcc tgcc 14

<210> 8  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 bases of Intron 1

<400> 8  
 aaagagggtg gctg 14

<210> 9  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last 7 bases of Intron 1

<400> 9  
 aacagaagcc gagc 14

<210> 10  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 bases of Intron Alpha

<400> 10

tgtcaagggtg gatg 14

<210> 11  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last 7 bases of Intron Alpha

<400> 11  
 cccccaggac aggc 14

<210> 12  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 bases of Intron Beta

<400> 12  
 gagccacgtc tcta 14

<210> 13  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (1)..(7)  
 <223> Last 7 bases of Intron Beta

<400> 13  
 ggggcaagtc ctac 14

<210> 14  
 <211> 14  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> intron  
 <222> (8)..(14)  
 <223> First 7 base of Intron 2

<400> 14  
 actccagggtg agcg 14

<210> 15  
 <211> 14  
 <212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1)..(7)

<223> Wherein N is any nucleotide

<220>

<221> intron

<222> (1)..(7)

<223> Last 7 bases of Intron 2

<400> 15

nnnnnnncta tgcc

14

<210> 16

<211> 173

<212> DNA

<213> Homo sapiens

<220>

<221> intron

<222> (8)..(166)

<223> Full Sequence of Intron 3

<400> 16

aacgcagccg aagaaaacat ttctgtcgtg actcctgcgg tgcttgggtc gggacagcca 60  
gagatggagc caccgccgag accgtcgggt gtgggcagct ttccggtgtc tcctgggagg 120  
ggagttgggc tgggcctgtg actcctcagc ctctgttttc cccagggat gtc 173

<210> 17

<211> 46

<212> PRT

<213> Homo sapiens

<400> 17

Thr Ala Ala Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly  
1 5 10 15

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly  
20 25 30

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
35 40 45

<210> 18

<211> 104

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Y

<400> 18

ggcctccccg gggtcggcgt ccggctgggg ttgagggcgg ccggggggaa ccagcgacat 60  
gcggagagca gcgcaggcga ctcagggcgc ttccccgcga ggtg 104

<210> 19  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Reding Frame One of Intron Y

<400> 19  
 Gly Leu Pro Gly Val Gly Val Arg Leu Gly Leu Arg Ala Ala Gly Gly  
           1                  5                  10                  15  
 Asn Gln Arg His Ala Glu Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro  
                   20                  25                  30  
 Arg Arg

<210> 20  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Reading Frame Two of Intron Y before termination  
 Codon

<400> 20  
 Ala Ser Pro Gly Ser Ala Ser Gly Trp Gly  
           1                  5                  10

<210> 21  
 <211> 23  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Reading Frame Two of Intron Y after termination  
 Codon

<400> 21  
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
           1                  5                  10                  15

Gln Gly Ala Ser Pro Ala Gly  
                   20

<210> 22  
 <211> 34  
 <212> PRT  
 <213> Homo sapiens

<220>

<223> Reading Frame Three of Intron Y

<400> 22

Pro Pro Arg Gly Arg Arg Pro Ala Gly Val Glu Gly Gly Arg Gly Glu  
1 5 10 15

Pro Ala Thr Cys Gly Glu Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro  
20 25 30

Gln Val

<210> 23

<211> 38

<212> DNA

<213> Homo sapiens

<220>

<223> Intron 1

<400> 23

gtggctgtgc tttggtttta cttccttttt aaccagaa

38

<210> 24

<211> 13

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 1 Translation

<400> 24

Val Ala Val Leu Trp Phe Asn Phe Leu Phe Asn Gln Lys  
1 5 10

<210> 25

<211> 36

<212> DNA

<213> Homo sapiens

<220>

<223> Intron Alpha

<400> 25

gtggatgtga cgggcgcgta cgacaccatc cccag

36

<210> 26

<211> 12

<212> PRT

<213> Homo sapiens

<220>

<223> Intron Alpha Translation

<400> 26

Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln  
 1 5 10

<210> 27  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Intron Beta

<400> 27  
 gtctctacct tgacagacct ccagccgtac atgcgacagt tcgtggctca cctgcaggag 60  
 accagcccgc tgagggatgc cgtcgtcatc gagcagagct cctccctgaa tgaggccagc 120  
 agtggcctct tcgacgtctt cctacgcttc atgtgccacc acgccgtgcg catcaggggc 180  
 aa 182

<210> 28  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Intron Beta Translation

<400> 28  
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala  
 1 5 10 15

His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln  
 20 25 30

Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu  
 35 40 45

Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys  
 50 55 60

<210> 29  
 <211> 226  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Intron 2

<400> 29  
 gtgagcgcac ctggccggaa gtggagcctg tgcccggctg gggcagggtgc tgctgcaggg 60  
 ccgttgcgtc cacctctgct tccgtgtggg gcaggcgact gccaatccca aagggtcaga 120  
 tgccacaggg tgcccctcgt cccatctggg gctgagcaca aatgcatctt tctgtgggag 180  
 tgagggtgcc tcacaacggg agcagttttc tgtgctattt tggtaa 226

<210> 30  
 <211> 159  
 <212> DNA

<213> Homo sapiens

<220>

<223> Intron 3

<400> 30

```
ccgaagaaaa catttctgtc gtgactcctg cgggtgcttg gtcgggacag ccagagatgg 60
agccaccccg cagaccgtcg ggtgtgggca gctttccggt gtctcctggg aggggagttg 120
ggctgggcct gtgactcctc agcctctgtt ttccccag 159
```

<210> 31

<211> 44

<212> PRT

<213> Homo sapiens

<220>

<223> Intron 3 Translation

<400> 31

```
Ala Glu Glu Asn Ile Ser Val Val Thr Pro Ala Val Leu Gly Ser Gly
  1              5              10              15
```

```
Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe
          20          25          30
```

```
Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu
      35          40
```

<210> 32

<211> 262

<212> DNA

<213> Homo sapiens

<220>

<223> Intron X. Complete length unknown

<400> 32

```
gacagtcacc agggggggttg accgccggac tgggcgtccc caggggttgac tataggacca 60
ggtgtccagg tgccctgcaa gtagaggggc tctcagaggc gtctggctgg catgggtgga 120
cgtggccccc ggcattggcct tctgcgtgtg ctgccgtggg tgccctgagc cctcactgag 180
tcggtggggg cttgtggcct cccgtgagct tccccctagt ctgttgtctg gctgagcaag 240
cctcctgagg ggctctctat tg 262
```

<210> 33

<211> 218

<212> DNA

<213> Homo sapiens

<220>

<223> Partial Sequence of Genomic Intron (approximately 2.7 kb)

<400> 33

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gtggctgtgc tttggtttta cttccttttt aaccagaagt gcgtttgagc cccacatttg 60
gtatcagctt agatgaaggg cccggaggag gggccacggg acacagccag ggccatggca 120
cggcgccccc ccatttgtgc gcacagttag gtggccgagg tgccggtgcc tccagaaaag 180
```

cagcgtgggg gtgtaggggg agctcctggg gcagggac

218

<210> 34  
 <211> 2031  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1767)..(1769)  
 <223> Wherein N is A, C, G or T

<220>  
 <223> N-Terminal Truncated Telomerase

<400> 34

atgcgcgcgc	ctccccgctg	ccgagccgtg	cgctccctgc	tgcgcagcca	ctacgcgag	60
gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctggtgcag	120
cgcggggacc	cgcgggcttt	ccgcgcgctg	gtggcccagt	gcctggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgtcctgcct	gaaggagctg	240
gtggcccag	tgctgcagag	gctgtgcgag	cgcgggcgca	agaacgtgct	ggccttcggc	300
ttcgcgctgc	tggacggggc	ccgcgggggc	ccccccgagg	ccttcaccac	cagcgtgcgc	360
agctacctgc	ccaacacggt	gaccgacgca	ctgcggggga	gcggggctg	ggggctgctg	420
ctgcgcgcgc	tgggcgacga	cgtgctggtt	cacctgctgg	cacgctgcgc	gctctttgtg	480
ctggtggctc	ccagctgcgc	ctaccaggtg	tgcgggcccgc	cgctgtacca	gctcggcgct	540
gocactcagg	cccggccccc	gccacacgct	agtggacccc	gaaggcgtct	gggatgcgaa	600
cgggcctgga	accatagcgt	cagggaggcc	ggggctcccc	tgggcctgcc	agccccgggt	660
gcgaggaggc	gcgggggagc	tgccagccga	agtctgccgt	tgcccaagag	gcccaggcgt	720
ggcgtgccc	ctgagccgga	gcggacgccc	gttgggcagg	ggctcctggc	ccaccggggc	780
aggacgcgtg	gaccgagtg	ccgtgggttt	tgtgtggtgt	cacctgccag	acccgccgaa	840
gaagccacct	ctttggaggg	tgcgctctct	ggcacgcgcc	actcccaccc	atccgtgggc	900
cgccagcacc	acgcggggcc	cccattccaca	tgcgggccac	cacgtccctg	ggacacgcct	960
tgtcccccg	tgtacgcga	gaccaagcac	ttcctctact	cctcaggcga	caaggagcag	1020
ctgcggccct	ccttcctact	cagctctctg	aggcccagcc	tgactggcgc	tcggaggctc	1080
gtggagacca	tctttctggg	ttccaggccc	tggatgccag	ggactccccg	cagggtgccc	1140
cgctgcccc	agcgtactg	gcaaattgcg	cccctgtttc	tggagctgct	tgggaaccac	1200
gcgcagtgcc	cctacggggt	gctcctcaag	acgcactgcc	cgctgcgagc	tgcggtcacc	1260
ccagcagccg	gtgtctgtgc	ccgggagaag	ccccagggct	ctgtggcggc	ccccgaggag	1320
gaggacacag	acccccgtcg	cctggtgcag	ctgctccgcc	agcacagcag	ccccctggcag	1380
gtgtacggct	tcgtgcgggc	ctgcctgcgc	cggtggtgc	ccccaggcct	ctggggctcc	1440
aggcacaacg	aacgccgctt	cctcaggaa	accaaagaag	tcattctccct	ggggaagcat	1500
gccaagctct	cgctgcagga	gctgacgtgg	aagatgagcg	tgcgggactg	cgcttggtcg	1560
cgcaggagcc	caggggttgg	ctgtgttccg	gccgcagagc	accgtctgcg	tgaggagatc	1620
ctggccaagt	tctgcactg	gctgatgagt	gtgtacgtcg	tcgagctgct	caggctcttc	1680
ttttatgtca	cggagaccac	gtttcaaaag	aaacaggctct	ttttctaccg	gaagagtgtc	1740
tggagcaagt	tgcaaagcat	tgggaatnng	acagtcacca	gggggggtga	ccgccggact	1800
gggcgtcccc	agggttgact	ataggaccag	gtgtccagg	gccctgcaag	tagaggggct	1860
ctcagaggcg	tctggctggc	atgggtggac	gtggcccccg	gcatggcctt	ctgcgtgtgc	1920
tgcggtgggt	gccctgagcc	ctcactgagt	cggtgggggc	ttgtggcttc	ccgtgagctt	1980
ccccctagtc	tgttgtctgg	ctgagcaagc	ctcctgaggg	gctctctatt	g	2031

<210> 35  
 <211> 588  
 <212> PRT  
 <213> Homo sapiens

<220>

<223> Protein Predicted by SEQ ID NO:34

<400> 35

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 1 18 5 10 15  
 His (Thr) Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175  
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285

Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
 580 585

<210> 36  
 <211> 2041  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 1; Intron 1 Addition

<400> 36  
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 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180  
 gacgcacggc cgcgcgcgcg cgcgcctcc ttccgccagg tgcctgcct gaaggagctg 240  
 gtggcccagag tgcctgcagag gctgtgcgag cgcggcgcga agaacgtgct ggccttcggc 300  
 ttgcgcgtgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgctg ggggctgctg 420  
 ctgcgcgcgcg tgggcgacga cgtgctgggt cacctgctgg cacgctgcgc gctctttgtg 480  
 ctggtggctc ccagctgcgc ctaccagggtg tgcgggcgcg cgctgtacca gctcggcgct 540  
 gccactcagg cccggccccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600  
 cgggcctgga accatagcgt cagggaggcc ggggtcccc tgggcctgcc agccccgggt 660  
 gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gcccaggcgt 720  
 ggcgtgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccaccgggc 780  
 aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840  
 gaagccacct ctttggaggg tgcgtctctt ggcacgcgcc actccacccc atccgtgggc 900  
 cgccagcacc acgcgggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960  
 tgtccccgcg tgtacgcga gaccaagcac ttctctact cctcaggcga caaggagcag 1020  
 ctgcggccct ccttctact cagctctctg agggccagcc tgactggcgc tcggaggctc 1080  
 gtggagacca tctttctggg ttccaggccc tggatgccag ggactcccc caggttgccc 1140  
 cgctgcccc agcgtactg gcaaagtgcg cccctgtttc tggagctgct tgggaaccac 1200  
 gcgcagtgcc cctacggggt gctcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260  
 ccagcagccg gtgtctgtgc ccgggagaag cccagggct ctgtggcggc ccccgaggag 1320  
 gaggacacag acccccgctc cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380  
 gtgtacggt tcgtgcgggc ctgcctgcgc cggctggtgc cccaggcct ctggggctcc 1440  
 aggacacaag aacgcgcgtt cctcaggaa accaagaagt tcatctccct ggggaagcat 1500  
 gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggtg 1560  
 cgcaggagcc caggggttgg ctgtgttccg gccgcagagc accgtctgcg tgaggagatc 1620  
 ctggccaagt tctgcactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680  
 ttttatgtca cggagaccac gtttcaaaag aacaggctct ttttctaccg gaagagtgtc 1740  
 tggagcaagt tgcaaagcat tggaatcaga cagcacttga agagggtgca gctgcgggag 1800  
 ctgtcgggaag cagaggtcag gcagcatcgg gaagccaggc ccgcctgct gacgtccaga 1860  
 ctccgcttca tccccagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920  
 ggagccagaa cgttccgcag agaaaagagg gtggctgtgc tttggtttaa cttccttttt 1980  
 aaccagaagc cgagcgtctc acctcgaggg tgaaggcact gttcagcgtg ctcaactacg 2040  
 a 2041

<210> 37  
 <211> 670  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 1; Encoded by SEQ ID NO:36

<400> 37  
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175  
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620

Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
625 630 635 640

Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe  
645 650 655

Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly  
660 665 670

<210> 38  
<211> 2541  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Truncated Protein 2; Alpha Intron Addition

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cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180  
gacgcacggc cgccccccgc cgccccctcc ttccgccagg tgcctgcct gaaggagctg 240  
gtggccccgag tgctgcagag gctgtgcgag cgcggcgcga agaactgct ggccttcggc 300  
ttcgcgctgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgctg ggggctgctg 420  
ctgcgcgcgc tgggcgacga cgtgctggtt cactgctgg cacgctgcgc gctctttgtg 480  
ctggtggctc ccagctgcgc ctaccaggtg tgcgggccgc cgctgtacca gctcggcgct 540  
gccactcagg cccggcccc gccacacgct agtggacccc gaaggcgtct gggatgcgaa 600  
cgggcctgga accatagcgt caggaggccc ggggtcccc tgggcctgcc agccccgggt 660  
gcgaggaggc gcgggggcag tgccagccga agtctgccgt tgcccaagag gccaggcgt 720  
ggcgtgccc ctgagccgga gcggacgccc gttgggcagg ggtcctgggc ccaccgggc 780  
aggacgcgtg gaccgagtga ccgtggtttc tgtgtggtgt cacctgccag acccgccgaa 840  
gaagccacct ctttgagggt tgcgtctctt ggcacgcgcc actcccacc atcctgggc 900  
cgccagcacc acgcggggccc cccatccaca tcgcggccac cacgtccctg ggacacgcct 960  
tgtcccccg tgtacgccga gaccaagcac ttctctact cctcaggcga caaggagcag 1020  
ctgcggccct ccttctact cagctctctg aggccagcc tgactggcg tcggaggctc 1080  
gtggagacca tctttctggg ttccaggccc tggatgccag ggactcccc caggttgccc 1140  
cgctgcccc agcgtactg gcaaagtgcg cccctgtttc tggagctgct tgggaaccac 1200  
gcgcagtgcc cctacggggt gtcctcaag acgcactgcc cgctgcgagc tgcggtcacc 1260  
ccagcagccg gtgtctgtgc ccgggagaag cccagggtct ctgtggcggc cccgaggag 1320  
gaggacacag accccgctcg cctggtgcag ctgctccgcc agcacagcag cccctggcag 1380  
gtgtacggct tcgtgcgggc ctgcctgcgc cggctggtgc cccaggcct ctggggctcc 1440  
aggcacaacg aacgcgcgtt cctcaggaac accaagaagt tcatctccct ggggaagcat 1500  
gccaagctct cgctgcagga gctgacgtgg aagatgagcg tgcgggactg cgcttggtg 1560  
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ctggccaagt tctgcaactg gctgatgagt gtgtacgtcg tcgagctgct caggtctttc 1680  
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ctccgcttca tccccagcc tgacgggctg cggccgattg tgaacatgga ctacgtcgtg 1920  
ggagccagaa cgttccgcag agaaaagagg gccgagcgtc tcacctcgag ggtgaaggca 1980  
ctgttcagcg tgctcaacta cgagcgggcg cggcgccccg gcctcctggg cgctctgtg 2040  
ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcggggccag 2100  
gacccgccgc ctgagctgta ctttgtcaag gtggatgtga cgggcgcgta cgacaccatc 2160  
ccccaggaca ggctcacgga ggtcatcgcc agcatcatca aacccagaa cacgtactgc 2220

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gtgcgctcgggt atgccgtgggt ccagaaggcc gcccatgggc acgtccgcaa ggccttcaag 2280
agccacgtcc tacgtccagt gccaggggat cccgcagggc tccatcctct ccacgtgct 2340
ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc ggcgggacgg 2400
gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca cccacgcgaa 2460
aaccttcttc aggaccttg tccgaggtgt ccctgagtat ggctgcgtgg tgaacttgcg 2520
gaagacagtg gtgaacttcc c 2541

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<210> 39  
 <211> 806  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 2; Encoded by SEQ ID NO:38

<400> 39

Met	Pro	Arg	Ala	Pro	Arg	Cys	Arg	Ala	Val	Arg	Ser	Leu	Leu	Arg	Ser	1	5	10	15
His	Thr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	20	25	30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Ser	Cys	Leu	Lys	Glu	Leu	65	70	75	80
Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	85	90	95	
Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	100	105	110	
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	115	120	125	
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	130	135	140	
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	145	150	155	160
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	165	170	175	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	180	185	190	
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	195	200	205	
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	210	215	220	

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
 500 505 510  
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525

Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
 530 535 540  
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe  
 545 550 555 560  
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr  
 565 570 575  
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln  
 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
 610 615 620  
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
 625 630 635 640  
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
 645 650 655  
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
 660 665 670  
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
 675 680 685  
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700  
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
 705 710 715 720  
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
 725 730 735  
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
 740 745 750  
 Gly His Val Arg Lys Ala Phe Lys Ser Val Leu Arg Pro Val Pro Gly  
 755 760 765  
 Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu  
 770 775 780  
 Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala  
 785 790 795 800  
 Ala Pro Ala Phe Val Gly  
 805

<211> 3396  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Reference Telomerase; with Intron Alpha and Beta

<400> 40

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 cgcggggacc cggcgcttt ccgcgcgctg gtggcccagt gcctgggtgt cgtgccctgg 180  
 gacgcacggc cgcggggcgc cgcggcctcc ttccgccagg tgcctgcct gaaggagctg 240  
 gtggcccag tgcctgcagag gctgtgcgag cgcggcgcga agaactgct ggccttcggc 300  
 ttgcgcgtgc tggacggggc ccgcgggggc cccccgagg ccttcaccac cagcgtgcgc 360  
 agctacctgc ccaacacggt gaccgacgca ctgcggggga gcggggcgtg ggggctgctg 420  
 ttgcgcgcgc tggcgacga cgtgctggtt cactgtctgg cagcgtgcgc gctctttgtg 480  
 ctgggtggctc ccagctgcgc ctaccagggt tgcggggcgc cgctgtacca gctcggcgct 540  
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<212> DNA
<213> Homo sapiens

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<220>
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 <212> PRT  
 <213> Homo sapiens

<220>  
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 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
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 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
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Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
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 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
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 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
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 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
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 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
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 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
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 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
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 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
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 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
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Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
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 690 695 700  
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
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 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
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 740 745 750  
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
 755 760 765  
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
 770 775 780

Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
785 790 795 800

Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
805 810 815

Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
820 825 830

Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
835 840 845

Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
850 855 860

Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
865 870 875 880

Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
885 890 895

Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
900 905 910

Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe  
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<211> 3362  
<212> DNA  
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<220>  
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 ga 3362

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 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
 115 120 125  
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130 135 140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145 150 155 160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165 170 175  
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180 185 190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195 200 205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210 215 220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225 230 235 240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245 250 255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260 265 270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320

Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355 360 365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385 390 395 400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
 435 440 445  
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe  
 450 455 460  
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser  
 465 470 475 480  
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser  
 485 490 495  
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met  
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
 515 520 525  
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
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 545 550 555 560  
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 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
 580 585 590  
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 595 600 605  
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
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Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val  
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 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser  
 645 650 655  
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg  
 660 665 670  
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg  
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 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro  
 690 695 700  
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile  
 705 710 715 720  
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln  
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 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His  
 740 745 750  
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp  
 755 760 765  
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser  
 770 775 780  
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu  
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 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His  
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 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro  
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 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp  
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 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu  
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 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala  
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 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys  
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 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu  
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Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser  
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Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe  
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Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly  
965 970 975

Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn  
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Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln  
995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln  
1010 1015 1020

Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala  
1025 1030 1035 1040

Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn  
1045 1050 1055

Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met  
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Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser Pro  
1075 1080 1085

Gly Arg Gly Val Gly Leu Gly Leu  
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<210> 45  
<211> 3918  
<212> DNA  
<213> Homo sapiens

<220>  
<223> Protein that lacks Motif A; with Intron Beta

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cgcggggacc cggcggttt cgcgcgcgtg gtggcccagt gcctggtgtg cgtgccctgg 180  
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TAC

||

tyrosine

||

Y

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 <211> 1120  
 <212> PRT

<213> Homo sapiens

<220>

<223> Protein that lacks Motif A; Encoded by SEQ ID  
NO:45

<400> 46

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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
65 70 75 80

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
85 90 95

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
100 105 110

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
115 120 125

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
145 150 155 160

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
165 170 175

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
180 185 190

Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
195 200 205

Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
210 215 220

Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
225 230 235 240

Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
245 250 255

Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
260 265 270

Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275 280 285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290 295 300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305 310 315 320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325 330 335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340 345 350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
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 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370 375 380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
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 405 410 415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln  
 420 425 430  
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu  
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 465 470 475 480  
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 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys  
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 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe  
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Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His  
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 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile  
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 Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys  
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 Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His  
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 Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro  
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Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro  
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 Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala  
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 His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu  
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 Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala  
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 Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg  
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 Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp  
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 Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile  
 980 985 990  
 Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro  
 995 1000 1005  
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 His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln  
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 Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu  
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<210> 47  
 <211> 3033  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein that lacks Motif A; with Introns

## Beta and 2

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 gccggaagtg gagcctgtgc ccggtggtg caggtgctgc tgcagggccg ttgcgtccac 2880  
 ctctgcttcc gtgtggggca ggcgactgcc aatcccaaag ggtcagatgc cacagggtgc 2940  
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&lt;210&gt; 48

&lt;211&gt; 936

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Truncated Protein that lacks Motif A; Encoded by  
SEQ ID NO:47

&lt;400&gt; 48

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
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Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60  
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
65 70 75 80  
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
85 90 95  
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
100 105 110  
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr  
115 120 125  
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
130 135 140  
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
145 150 155 160  
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
165 170 175  
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
180 185 190  
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
195 200 205  
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
210 215 220  
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
225 230 235 240  
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
245 250 255  
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val

			260				265				270				
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Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly
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Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln
		370				375					380				
Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His
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Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg
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Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr	Gly	Phe
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Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp	Gly	Ser
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Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe	Ile	Ser
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Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp	Lys	Met
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Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys
		515					520					525			
Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe
		530				535					540				
Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe
		545			550					555					
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr

565					570					575					
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Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln
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His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile
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Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val
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Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser
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Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg
			660					665					670		
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg
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Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro
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Glu	Leu	Tyr	Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile
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Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln
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Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser
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Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu
		755					760					765			
Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser
	770					775					780				
Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe
	785					790					795			800	
Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys
				805					810					815	
Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu
			820					825					830		
Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp
		835					840					845			
Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His
	850					855					860				
Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro



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 ctgggcctgg acgatatcca cagggcctgg cgcaccttcg tgctgcgtgt gcgggcccag 2100  
 gaccgcgcgc ctgagctgta ctttgtcaag gacaggctca cggaggtcat cgccagcatc 2160  
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<210> 50  
 <211> 1084  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus;  
 Encoded by SEQ ID NO:49

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 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu  
 65 70 75 80  
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val  
 85 90 95  
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro  
 100 105 110  
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

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 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val  
 130                      135                      140  
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val  
 145                      150                      155                      160  
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr  
 165                      170                      175  
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly  
 180                      185                      190  
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg  
 195                      200                      205  
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg  
 210                      215                      220  
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg  
 225                      230                      235                      240  
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp  
 245                      250                      255  
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val  
 260                      265                      270  
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala  
 275                      280                      285  
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His  
 290                      295                      300  
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro  
 305                      310                      315                      320  
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly  
 325                      330                      335  
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro  
 340                      345                      350  
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser  
 355                      360                      365  
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln  
 370                      375                      380  
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His  
 385                      390                      395                      400  
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg  
 405                      410                      415  
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln

✓

725								730								735							
Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser								
740								745				750											
Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu								
755								760				765											
Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser								
770				775				780															
Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe								
785				790				795				800											
Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys								
805								810				815											
Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu								
820								825				830											
Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp								
835				840				845															
Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His								
850				855				860															
Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro								
865				870				875				880											
Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro								
885				890				895															
Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala								
900				905				910															
His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu								
915				920				925															
Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	Arg	Ala								
930				935				940															
Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	Arg	Arg								
945				950				955				960											
Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	Leu	Asp								
965				970				975															
Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile								
980				985				990															
Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro								
995				1000				1005															
Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile								
1010				1015				1020															
Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala								

1025                      1030                      1035                      1040

Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly  
                                  1045                      1050                      1055

Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe  
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Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
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<210> 51  
 <211> 2135  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1871)..(1873)  
 <223> Wherein N is A, C, G or T

<220>  
 <223> N-Terminal Truncated Telomerase (ver. 2); with  
 Intron Y

<400> 51

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cgcggggacc	cggcggcttt	ccgcgcgctg	gtggcccagt	gcctgggtgtg	cgtgcccttg	180
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cgagcgggac	gcccgttggg	caggggtcct	ggggccaccc	gggcaggacg	cgtaggaccga	900
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<210> 52  
 <211> 622  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> N-Terminal Truncated Telomerase (ver.2); encoded  
 by SEQ ID NO:51 and ORF1 of Intron Y

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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
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 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
 65 70 75 80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
 85 90 95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
 145 150 155 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala

210						215						220					
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225					230					235					240		
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg		
				245					250					255			
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro		
			260					265					270				
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly		
		275					280					285					
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe		
	290					295					300						
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu		
305					310					315					320		
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln		
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His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp		
			340					345					350				
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser		
		355					360					365					
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu		
	370					375					380						
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu		
385					390					395					400		
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu		
			405					410						415			
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly		
			420					425					430				
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro		
		435					440					445					
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys		
	450					455					460						
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg		
465					470					475					480		
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr		
				485					490					495			
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp		
		500						505					510				
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe		

515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp 530 535 540		
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val 545 550 555 560		
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala 565 570 575		
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg 580 585 590		
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe 595 600 605		
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly 610 615 620		

<210> 53  
 <211> 84  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Splicing Variant of Human Telomerase encoded by  
 Intron Y, ORF2, before the termination codon.  
 SEQ ID NOs: 51,55,59,63,67,71,75,79,83 encode this  
 fragment

<400> 53
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser 1 5 10 15
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly 20 25 30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg 35 40 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro 50 55 60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ala Ser Pro Gly Ser Ala 65 70 75 80
Ser Gly Trp Gly

<210> 54  
 <211> 537  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

<223> N-Terminal Truncated Telomerase (ver. 2); encoded  
by SEQ ID NO:51, with Y intron, ORF2, after the  
termination codon

&lt;400&gt; 54

Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
180 185 190

Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
195 200 205

Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
225 230 235 240

Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
245 250 255

Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
260 265 270

Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly  
 530 535

<210> 55  
 <211> 2145  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;223&gt; Truncated Protein 1 (ver.2); with Introns Y and 1

&lt;400&gt; 55

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atgccgcgcg ctccccgctg ccgagccgtg cgctccctgc tgcgcagcca ctaccgcgag 60
gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctgggtgcag 120
cgcgggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180
gacgcacggc cgcggggggc cgccccctcc ttccgccagg tgggcctccc cggggtcggc 240
gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300
gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgtctc 360
agaggctgtg cgagcgcggc gcgaagaacg tctggcctt cggcttcgcg ctgtggagc 420
gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgccaaca 480
cgggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgtctgcg cgcgtggcg 540
acgacgtgct ggttcacctg ctggcacgct gcgcgtctt tgtgtgtgtg gctcccagct 600
gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggcccggc 660
ccccgccaca cgctagtggc cccgaaggc gtctgggatg cgaacgggcc tggaccata 720
gcgtcagggg ggccgggggt cccctgggccc tggcagcccc ggggtgcgag aggcgcggg 780
gcagtgccag ccgaagtctg ccgttgccca agaggccag gcgtggcgct gcccctgagc 840
cggagcggac gcccgttggg caggggtcct gggccacccc gggcaggacg cgtggaccga 900
gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttg 960
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ccgagacca gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140
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tgggttccag gccctggatg ccagggactc cccgcagggt gccccgcctg cccagcgt 1260
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gtgcccggga gaagccccag ggctctgtgg cggccccga ggaggaggac acagaccccc 1440
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gggcctgct gcgcgggtg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560
gcttctcag gaacaccaag aagttcatct ccctggggaa gcatgccaag ctctcgtgc 1620
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ttggtgtgt tccggccgca gagcacgtc tgcgtgagga gatcctggcc aagttcctgc 1740
actggctgat gagtgtgtac gtcgtcagc tgcctaggct tttcttttat gtcacggaga 1800
ccagtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860
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tcaggcagca tcgggaagcc aggccgccc tgcgtacgtc cagactccgc ttcacccca 1980
agcctgacgg gctgcggcgg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040
gcagagaaaa gaggtgggt gtgctttggt ttaacttct ttttaaccag aagccgagcg 2100
tctcacctcg aggggtgaagg cactgttcag cgtgctcaac tacga 2145

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&lt;210&gt; 56

&lt;211&gt; 704

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Truncated Protein 1 (ver.2); encoded by SEQ ID  
NO:55, with Y Intron ORF1

&lt;400&gt; 56

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Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20              25              30

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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
                   35                                  40                                  45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
           50  55                                  60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
   65  70                                  75                                  80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
                                   85                                  90                                  95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
                   100                                  105                                  110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
           115                                  120                                  125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
   130                                  135                                  140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
  145                                  150                                  155                                  160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
                   165                                  170                                  175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
                   180                                  185                                  190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
   195                                  200                                  205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
   210                                  215                                  220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
  225                                  230                                  235                                  240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
                   245                                  250                                  255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
                   260                                  265                                  270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
           275                                  280                                  285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
   290                                  295                                  300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
  305                                  310                                  315                                  320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
                   325                                  330                                  335

His 340	His 340	Ala 340	Gly 340	Pro 340	Pro 340	Ser 340	Thr 340	Ser 345	Arg 345	Pro 345	Pro 345	Arg 350	Pro 350	Trp 350	Asp 350
Thr 355	Pro 355	Cys 355	Pro 355	Pro 355	Val 355	Tyr 355	Ala 360	Glu 360	Thr 360	Lys 360	His 365	Phe 365	Leu 365	Tyr 365	Ser 365
Ser 370	Gly 370	Asp 370	Lys 370	Glu 370	Gln 370	Leu 375	Arg 375	Pro 375	Ser 375	Phe 380	Leu 380	Leu 380	Ser 380	Ser 380	Leu 380
Arg 385	Pro 385	Ser 385	Leu 385	Thr 385	Gly 390	Ala 390	Arg 390	Arg 390	Leu 395	Val 395	Glu 395	Thr 395	Ile 395	Phe 400	Leu 400
Gly 410	Ser 410	Arg 410	Pro 410	Trp 405	Met 405	Pro 410	Gly 410	Thr 410	Pro 410	Arg 410	Arg 410	Leu 415	Pro 415	Arg 415	Leu 415
Pro 420	Gln 420	Arg 420	Tyr 420	Trp 420	Gln 420	Met 420	Arg 425	Pro 425	Leu 425	Phe 425	Leu 425	Glu 430	Leu 430	Leu 430	Gly 430
Asn 435	His 435	Ala 435	Gln 435	Cys 435	Pro 435	Tyr 435	Gly 440	Val 440	Leu 440	Leu 440	Lys 445	Thr 445	His 445	Cys 445	Pro 445
Leu 450	Arg 450	Ala 450	Ala 450	Val 450	Thr 450	Pro 455	Ala 455	Ala 455	Gly 455	Val 455	Cys 460	Ala 460	Arg 460	Glu 460	Lys 460
Pro 465	Gln 465	Gly 465	Ser 465	Val 465	Ala 470	Ala 470	Pro 470	Glu 470	Glu 475	Glu 475	Asp 475	Thr 475	Asp 475	Pro 480	Arg 480
Arg 490	Leu 490	Val 490	Gln 490	Leu 485	Leu 485	Arg 485	Gln 490	His 490	Ser 490	Ser 490	Pro 490	Trp 495	Gln 495	Val 495	Tyr 495
Gly 500	Phe 500	Val 500	Arg 500	Ala 500	Cys 500	Leu 500	Arg 505	Arg 505	Leu 505	Val 505	Pro 505	Pro 510	Gly 510	Leu 510	Trp 510
Gly 515	Ser 515	Arg 515	His 515	Asn 515	Glu 515	Arg 515	Arg 520	Phe 520	Leu 520	Arg 520	Asn 525	Thr 525	Lys 525	Lys 525	Phe 525
Ile 530	Ser 530	Leu 530	Gly 530	Lys 530	His 535	Ala 535	Lys 535	Leu 535	Ser 535	Leu 535	Gln 540	Glu 540	Leu 540	Thr 540	Trp 540
Lys 545	Met 545	Ser 545	Val 545	Arg 545	Asp 550	Cys 550	Ala 550	Trp 550	Leu 555	Arg 555	Arg 555	Ser 555	Pro 555	Gly 560	Val 560
Gly 565	Cys 565	Val 565	Pro 565	Ala 565	Ala 565	Glu 565	His 565	Arg 570	Leu 570	Arg 570	Glu 570	Glu 570	Ile 575	Leu 575	Ala 575
Lys 580	Phe 580	Leu 580	His 580	Trp 580	Leu 580	Met 580	Ser 585	Val 585	Tyr 585	Val 585	Val 585	Glu 590	Leu 590	Leu 590	Arg 590
Ser 595	Phe 595	Phe 595	Tyr 595	Val 595	Thr 595	Glu 595	Thr 600	Thr 600	Phe 600	Gln 600	Lys 605	Asn 605	Arg 605	Leu 605	Phe 605
Phe 610	Tyr 610	Arg 610	Lys 610	Ser 610	Val 610	Trp 615	Ser 615	Lys 615	Leu 615	Gln 615	Ser 620	Ile 620	Gly 620	Ile 620	Arg 620
Gln 625	His 625	Leu 625	Lys 625	Arg 625	Val 630	Gln 630	Leu 630	Arg 630	Glu 635	Leu 635	Ser 635	Glu 635	Ala 635	Glu 640	Val 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
645 650 655

Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
660 665 670

Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu  
675 680 685

Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly  
690 695 700

<210> 57  
<211> 619  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Truncated Protein 1 (ver.2): encoded by SEQ ID  
NO:55, with Intron Y ORF2 after the termination  
codon

<400> 57  
Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
485 490 495

Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
500 505 510

Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
530 535 540

Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
545 550 555 560

Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
565 570 575

Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
580 585 590

Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu Trp Phe Thr Phe Leu  
595 600 605

Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly  
610 615

<210> 58  
<211> 704  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Truncated Protein 1 (ver.2); encoded by SEQ ID  
NO:55, with Intron Y ORF3

<400> 58  
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
65 70 75 80

Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu

85					90					95					
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys
			100					105					110		
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys
		115					120					125			
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly
	130					135					140				
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr
	145					150					155				160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg
				165					170					175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu
			180					185					190		
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro
		195					200					205			
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
	210					215					220				
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
	225					230					235				240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
			260					265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
			275				280					285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
	290					295					300				
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
	305					310					315				320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
			340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
		355					360					365			
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
	370					375					380				
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu

385		390		395		400
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu						
		405		410		415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly						
		420		425		430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro						
		435		440		445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys						
		450		455		460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg						
		465		470		475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr						
		485		490		495
Gly Phe Val Arg Ala Cys Leu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe						
		500		505		510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe						
		515		520		525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp						
		530		535		540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val						
		545		550		555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala						
		565		570		575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg						
		580		585		590
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe						
		595		600		605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg						
		610		615		620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val						
		625		630		635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg						
		645		650		655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr						
		660		665		670
Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Val Ala Val Leu						
		675		680		685
Trp Phe Thr Phe Leu Phe Asn Gln Lys Pro Ser Val Ser Phe Arg Gly						

690

695

700

<210> 59  
 <211> 2645  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 2 (ver.2); with Intron Y and  
 Alpha

<400> 59  
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 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctgggtgtg cgtgccctgg 180  
 gacgcacggc cggccccgcg cggccccctc ttccgccagg tgggcctccc cggggtcggc 240  
 gtccggctgg gggttagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300  
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctgggtggc cgagtgcctg 360  
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420  
 gggcccgcgg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgcccaca 480  
 cggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540  
 acgacgtgct gggtcacctg ctggcacgct gcgcgctctt tgtgctgggt gctcccagct 600  
 gcgcctacca ggtgtgcggg ccgcgcgtgt accagctcgg cgtgccact caggcccggc 660  
 ccccgccaca cgctagtga ccccggaagg gtctgggatg cgaacgggccc tggaaaccata 720  
 gcgtcaggga ggccgggggt cccctggggc tgccagcccc ggggtgcgag aggcgcgggg 780  
 gcagtgccag ccgaagtctg ccgttgccca agagycaccg gcgtggcgct gccctgagc 840  
 cggagcggac gcccgttggg caggggtcct gggcccaccc gggcaggacg cgtggaccga 900  
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgcg cgaagaagcc acctctttgg 960  
 aggggtgcgt ctctggcacg cggcactccc acccatccgt gggccgccag caccacgcgg 1020  
 gcccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080  
 ccgagaccaa gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140  
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200  
 tgggttccag gccctggatg ccagggactc cccgcagggt gccccgcctg cccagcgct 1260  
 actggcaaat gcggccccctg tttctggagc tgcttgggaa ccacgcgcag tgcccctacg 1320  
 ggggtgctcct caagacgcac tgcccgtgcg gagctgcggt caccacagca gccggtgtct 1380  
 gtgcccggga gaagccccag ggctctgtgg cggcccccca ggaggaggac acagaccccc 1440  
 gtgcctgggt gcagctgctc cgccagcaca gcagcccctg gcaggtgtac ggcttcgtgc 1500  
 gggcctgcct gcgcgggctg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560  
 gcttctcag gaacaccaag aagttcatct cctggggaa gcatgccaag ctctcgctgc 1620  
 aggagctgac gtggaagatg agcgtgcggg actgcgcttg gctgcgcagg agcccagggg 1680  
 ttggctgtgt tccggccgca gagcaccgtc tgctgagga gatcctggcc aagttcctgc 1740  
 actggctgat gagtgtgtac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800  
 ccacgtttca aaagaacagg ctctttttct accggaagag tgtctggagc aagttgcaaa 1860  
 gcattggaat cagacagcac ttgaagaggg tgcagctgcg ggagctgtcg gaagcagagg 1920  
 tcaggcagca tcgggaagcc agggccgccc tgctgacgtc cagactccgc ttcacccca 1980  
 agcctgacgg gctgcggcg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040  
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100  
 actacgagcg ggcgcggcgc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160  
 tccacagggc ctggcgcacc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220  
 tgtactttgt caaggtggat gtgacgggcg cgtacgacac catccccag gacaggctca 2280  
 cggaggtcat cgcagcacc atcaaaccac agaacacgta ctgcgtgcgt cggatgccc 2340  
 tgggtccagaa ggccgcccac gggcacgtcc gcaaggcctt caagagccac gtcctacgtc 2400  
 cagtgcacgg ggatcccga gggctccatc ctctccacgc tgctctgcag cctgtgctac 2460

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ggcgacatgg agaacaagct gtttgcgggg attcggcggg acgggctgct cctgcgtttg 2520
gtggatgatt tcttgttggg gacacctcac ctcaccacg cgaaaacctt cctcaggacc 2580
ctggtccgag gtgtccctga gtatggctgc gtggagaact tgcggaagac agtggagaac 2640
ttccc                                     2645

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<210> 60

<211> 841

<212> PRT

<213> Homo sapiens

<220>

<223> Truncated Protein 2 (ver.2); encoded by SEQ ID  
NO:59, with Intron Y ORF1

<400> 60

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Met  Pro  Arg  Ala  Pro  Arg  Cys  Arg  Ala  Val  Arg  Ser  Leu  Leu  Arg  Ser
  1              5              10              15

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His  Thr  Arg  Glu  Val  Leu  Pro  Leu  Ala  Thr  Phe  Val  Arg  Arg  Leu  Gly
              20              25              30

```

```

Pro  Gln  Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
              35              40              45

```

```

Ala  Leu  Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
  50              55              60

```

```

Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Gly  Leu  Pro  Gly  Val  Gly
  65              70              75              80

```

```

Val  Arg  Leu  Gly  Leu  Arg  Ala  Ala  Gly  Gly  Asn  Gln  Arg  His  Ala  Glu
              85              90              95

```

```

Ser  Ser  Ala  Gly  Asp  Ser  Gly  Arg  Phe  Pro  Arg  Arg  Ser  Cys  Leu  Lys
              100              105              110

```

```

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
              115              120              125

```

```

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
              130              135              140

```

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Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
              145              150              155              160

```

```

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
              165              170              175

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Arg  Val  Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
              180              185              190

```

```

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
              195              200              205

```

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Leu  Tyr  Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
              210              215              220

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Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525

Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765  
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro  
 785 790 795 800  
 Val Pro Gly Asp Pro Ala Gly Leu His Pro Leu His Ala Ala Leu Gln  
 805 810 815  
 Pro Val Leu Arg Arg His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala  
 820 825 830

Gly Arg Ala Ala Pro Ala Phe Val Gly  
835 840

<210> 61  
<211> 756  
<212> PRT  
<213> Homo sapiens

<220>  
<223> Truncated Protein 2 (ver.2); encoded by SEQ ID  
NO:59 with Intron Y ORF2 after the termination  
codon

<400> 61  
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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
20 25 30  
Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
35 40 45  
Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
50 55 60  
Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
65 70 75 80  
Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
85 90 95  
Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
100 105 110  
Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
115 120 125  
Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
130 135 140  
Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
145 150 155 160  
Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
165 170 175  
Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
180 185 190  
Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
195 200 205  
Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
210 215 220

Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525

Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540  
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp  
 660 665 670  
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr  
 675 680 685  
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val  
 690 695 700  
 Arg Lys Ala Phe Lys Ser His Val Leu Arg Pro Val Pro Gly Asp Pro  
 705 710 715 720  
 Ala Gly Leu His Pro Leu His Ala Ala Leu Gln Pro Val Leu Arg Arg  
 725 730 735  
 His Gly Glu Gln Ala Val Cys Gly Asp Ser Ala Gly Arg Ala Ala Pro  
 740 745 750  
 Ala Phe Val Gly  
 755

<210> 62  
 <211> 841  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 2 (ver.2); encoded by SEQ ID NO:  
 59 with Intron Y ORF3

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Pro Gln Gly	Trp Arg Leu Val Gln Arg Gly Asp	Pro Ala Ala Phe Arg	
	35	40	45
Ala Leu Val	Ala Gln Cys Leu Val Cys Val Pro Trp Asp	Ala Arg Pro	
	50	55	60
Pro Pro Ala	Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg		
	65	70	75
Pro Ala Gly	Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu		
	85	90	95
Gln Arg Arg	Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys		
	100	105	110
Glu Leu Val	Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys		
	115	120	125
Asn Val Leu	Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly		
	130	135	140
Pro Pro Glu	Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr		
	145	150	155
Val Thr Asp	Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg		
	165	170	175
Arg Val Gly	Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu		
	180	185	190
Phe Val Leu	Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro		
	195	200	205
Leu Tyr Gln	Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala		
	210	215	220
Ser Gly Pro	Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser		
	225	230	235
Val Arg Glu	Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg		
	245	250	255
Arg Arg Gly	Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro		
	260	265	270
Arg Arg Gly	Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly		
	275	280	285
Ser Trp Ala	His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe		
	290	295	300
Cys Val Val	Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu		

305		310		315		320									
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
			340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
		355					360					365			
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
	370					375					380				
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu
385					390					395					400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu
				405					410					415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly
			420					425					430		
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro
		435					440					445			
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys
	450					455					460				
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg
465					470					475					480
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr
				485					490					495	
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp
			500					505					510		
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe
		515					520					525			
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp
	530					535					540				
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val
545					550					555					560
Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala
				565					570					575	
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg
			580					585					590		
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe
		595					600					605			
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg

610					615					620					
Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val
625					630					635					640
Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg
				645					650					655	
Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr
			660					665					670		
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu
		675					680					685			
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
705					710					715					720
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
				725					730					735	
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp
			740					745					750		
Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys
		755					760					765			
Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala
		770				775					780				
Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Leu	Arg	Pro
785					790					795					800
Val	Pro	Gly	Asp	Pro	Ala	Gly	Leu	His	Pro	Leu	His	Ala	Ala	Leu	Gln
				805					810					815	
Pro	Val	Leu	Arg	Arg	His	Gly	Glu	Gln	Ala	Val	Cys	Gly	Asp	Ser	Ala
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Gly	Arg	Ala	Ala	Pro	Ala	Phe	Val	Gly							
		835					840								

<210> 63  
 <211> 3500  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Reference Protein (ver.2); with Introns Y, Alpha  
 and Beta

<400> 63  
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 gtgctgccgc tggccacgtt cgtgcggcgc ctggggcccc agggctggcg gctggtgcag 120

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 <213> Homo sapiens

<220>

<223> Reference Protein (ver.2); encoded by SEQ ID NO:63  
 with Intron Y ORF1

<400> 64

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Ser  Gly  Pro  Arg  Arg  Arg  Leu  Gly  Cys  Glu  Arg  Ala  Trp  Asn  His  Ser
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Val  Arg  Glu  Ala  Gly  Val  Pro  Leu  Gly  Leu  Pro  Ala  Pro  Gly  Ala  Arg

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Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
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Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
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Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
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Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val

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Ser Phe Phe	Tyr 595	Val Thr Glu Thr	Thr 600	Phe Gln Lys Asn	Arg 605	Leu Phe
Phe Tyr Arg	Lys 610	Ser Val Trp Ser	Lys 615	Leu Gln Ser Ile	Gly 620	Ile Arg
Gln His Leu	Lys 625	Arg Val Gln Leu	Arg 630	Glu Leu Ser Glu	Ala 635	Glu Val
Arg Gln His	Arg 645	Glu Ala Arg Pro	Ala 650	Leu Leu Thr Ser	Arg 655	Leu Arg
Phe Ile Pro	Lys 660	Pro Asp Gly Leu	Arg 665	Pro Ile Val Asn	Met 670	Asp Tyr
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Thr Ser Arg	Val 690	Lys Ala Leu Phe	Ser 695	Val Leu Asn Tyr	Glu 700	Arg Ala
Arg Arg Pro	Gly 705	Leu Leu Gly Ala	Ser 710	Val Leu Gly Leu	Asp 715	Asp Ile
His Arg Ala	Trp 725	Arg Thr Phe Val	Leu 730	Arg Val Arg Ala	Gln 735	Asp Pro
Pro Pro Glu	Leu 740	Tyr Phe Val Lys	Val 745	Asp Val Thr Gly	Ala 750	Tyr Asp
Thr Ile Pro	Gln 755	Asp Arg Leu Thr	Glu 760	Val Ile Ala Ser	Ile 765	Ile Lys
Pro Gln Asn	Thr 770	Tyr Cys Val Arg	Arg 775	Tyr Ala Val Val	Gln 780	Lys Ala
Ala His Gly	His 785	Val Arg Lys Ala	Phe 790	Lys Ser His Val	Ser 795	Thr Leu
Thr Asp Leu	Gln 805	Pro Tyr Met Arg	Gln 810	Phe Val Ala His	Leu 815	Gln Glu
Thr Ser Pro	Leu 820	Arg Asp Ala Val	Val 825	Ile Glu Gln Ser	Ser 830	Ser Leu
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His His Ala	Val 850	Arg Ile Arg Gly	Lys 855	Ser Tyr Val Gln	Cys 860	Gln Gly

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Asp Glu Ala Leu Gly 945	Gly Thr Ala Phe Val 950	Gln Met Pro Ala His Gly 955
Leu Phe Pro Trp Cys 965	Gly Leu Leu Leu 970	Asp Thr Arg Thr Leu Glu Val 975
Gln Ser Asp Tyr 980	Ser Ser Tyr Ala 985	Arg Thr Ser Ile Arg Ala Ser Leu 990
Thr Phe Asn Arg Gly 995	Phe Lys Ala 1000	Gly Arg Asn Met Arg Arg Lys Leu 1005
Phe Gly Val Leu Arg 1010	Leu Lys Cys His 1015	Ser Leu Phe Leu Asp Leu Gln 1020
Val Asn Ser Leu Gln 1025	Thr Val Cys Thr 1030	Asn Ile Tyr Lys Ile Leu Leu 1035
Leu Gln Ala Tyr Arg 1045	Phe His Ala Cys 1050	Val Leu Gln Leu Pro Phe His 1055
Gln Gln Val Trp Lys 1060	Asn Pro Thr Phe 1065	Phe Leu Arg Val Ile Ser Asp 1070
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Leu Gly Ala Lys Gly 1090	Ala Ala Gly 1095	Pro Leu Pro Ser Glu Ala Val Gln 1100
Trp Leu Cys His Gln 1105	Ala Phe Leu Leu 1110	Lys Leu Thr Arg His Arg Val 1115
Thr Tyr Val Pro Leu 1125	Leu Gly Ser Leu Arg 1130	Thr Ala Gln Thr Gln Leu 1135
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1155

1160

1165

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<223> Reference Protein (ver.2); encoded by SEQ ID NO:63  
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Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp
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Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg
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Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala
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Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro
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 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
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 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
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 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
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 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
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Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	His	Gly	His	Val
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Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro
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Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg
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Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser
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Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser
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Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn
785					790					795					800
Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val
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Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe
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Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn
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 885 890 895  
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly  
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 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg  
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 Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn Ser Leu Gln  
 930 935 940  
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg  
 945 950 955 960  
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys  
 965 970 975  
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys  
 980 985 990  
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu Gly Ala Lys  
 995 1000 1005  
 Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp Leu Cys His  
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 Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr Tyr Val Pro  
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<220>  
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 with Intron Y ORF3

<400> 66

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His	Tyr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly	20	25	30	
Pro	Gln	Gly	Trp	Arg	Leu	Val	Gln	Arg	Gly	Asp	Pro	Ala	Ala	Phe	Arg	35	40	45	
Ala	Leu	Val	Ala	Gln	Cys	Leu	Val	Cys	Val	Pro	Trp	Asp	Ala	Arg	Pro	50	55	60	
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Pro	Pro	Arg	Gly	Arg	Arg	65	70	75	80
Pro	Ala	Gly	Val	Glu	Gly	Gly	Arg	Gly	Glu	Pro	Ala	Thr	Cys	Gly	Glu	85	90	95	
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys	100	105	110	
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	115	120	125	
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	130	135	140	
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	145	150	155	160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	165	170	175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205	
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220	
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235	240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	260	265	270	
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	275	280	285	
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	290	295	300	

Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605

Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765  
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu  
 785 790 795 800  
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu  
 805 810 815  
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu  
 820 825 830  
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys  
 835 840 845  
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly  
 850 855 860  
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr  
 865 870 875 880  
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu  
 885 890 895  
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr  
 900 905 910

His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr  
           915                                  920                                  925  
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu  
           930                                  935                                  940  
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly  
   945                                  950                                  955                                  960  
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val  
                                   965                                  970                                  975  
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu  
                                   980                                  985                                  990  
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu  
                                   995                                  1000                                  1005  
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln  
   1010                                  1015                                  1020  
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu  
  1025                                  1030                                  1035                                  1040  
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His  
                                   1045                                  1050                                  1055  
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp  
                                   1060                                  1065                                  1070  
 Thr Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser  
   1075                                  1080                                  1085  
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln  
  1090                                  1095                                  1100  
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val  
  1105                                  1110                                  1115                                  1120  
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu  
                                   1125                                  1130                                  1135  
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala  
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 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
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<210> 67  
 <211> 3173  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein (ver.2); with Introns Y, Alpha,  
       Beta and 2

&lt;400&gt; 67

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gtgctgccgc	tggccacgtt	cgtgcggcgc	ctggggcccc	agggctggcg	gctgggtgcag	120
cgcggggacc	cggcggcttt	ccgcgcgctg	gtggcccagt	gcctgggtgtg	cgtgccctgg	180
gacgcacggc	cgccccccgc	cgccccctcc	ttccgccagg	tgggcctccc	cggggtcggc	240
gtccggctgg	ggttgagggc	ggccgggggg	aaccagcgac	atgcggagag	cagcgcaggc	300
gactcagggc	gcttcccccg	caggtgtcct	gcctgaagga	gctgggtggcc	cgagtgtctg	360
agaggctgtg	cgagcgcggc	gcgaagaacg	tgtggcctt	cggcttcgcg	ctgctggacg	420
gggcccgcgg	gggccccccc	gaggccttca	ccaccagcgt	gcgcagctac	ctgcccacaa	480
cggtgaccga	cgcactgcgg	gggagcgggg	cgtgggggct	gctgctgcgc	cgctggggcg	540
acgacgtgct	ggttcacctg	ctggcacgct	gcgcgctctt	tgtgctgggtg	gctcccagct	600
gcgccctacca	ggtgtgcggg	ccgcgcgctg	accagctcgg	cgctgccact	caggccccgc	660
ccccgccaca	cgctagtggg	ccccgaaggc	gtctgggatg	cgaacggggc	tggaaccata	720
gcgtcagggg	ggccgggggtc	cccctggggc	tgccagcccc	gggtgcgagg	aggcgcgggg	780
gcagtgccag	ccgaagtctg	ccgttgcccc	agaggcccag	gcgtggcgct	gccccctgac	840
cggagcggac	gcccgttggg	caggggtcct	gggcccaccc	gggcaggacg	cgtggaccga	900
gtgacgcgtg	tttctgtgtg	gtgtcacctg	ccagaccgcg	cgaagaagcc	acctcttttg	960
aggggtgcgt	ctctggcacg	cgccactccc	acccatccgt	gggcccgcag	caccacgcgg	1020
gccccccatc	cacatcgcg	ccaccacgtc	cctgggacac	gccttgtccc	ccggtgtacg	1080
ccgagaccaa	gcacttcctc	tactcctcag	gcgacaagga	gcagctgcgg	ccctccttcc	1140
tactcagctc	tctgaggccc	agcctgactg	gcgctcggag	gctcgtggag	accatctttc	1200
tgggttccag	gccctggatg	ccagggaactc	cccgacaggtt	gccccgcctg	ccccagcgtc	1260
actggcaaat	gcggccccctg	tttctggagc	tgcttgggaa	ccacgcgcag	tgccccctac	1320
gggtgctcct	caagacgcac	tgcccgcgtc	gagctgcggt	caccccagca	gccggtgtct	1380
gtgcccggga	gaagccccag	ggctctgttg	cgccccccga	ggaggaggac	acagaccccc	1440
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gcttctcag	gaacaccaag	aagttcatct	ccctggggaa	gcatgccaa	ctctcgctgc	1620
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ccacgtttca	aaagaacagg	ctctttttct	accggaagag	tgtctggagc	aagttgcaaa	1860
gcatttgaat	cagacagcac	ttgaagaggg	tgcagctgcg	ggagctgtcg	gaagcagagg	1920
tcaggcagca	tcgggaagcc	aggcccgcgc	tgtgacgtc	cagactccgc	ttcatcccca	1980
agcctgacgg	gctgcggccg	attgtgaaca	tggactacgt	cgtgggagcc	agaacgttcc	2040
gcagagaaaa	gagggccgag	cgtctcacct	cgagggtgaa	ggcactgttc	agcgtgctca	2100
actacgagcg	ggcgcggcgc	cccggcctcc	tgggcgcctc	tgtgctgggc	ctggacgata	2160
tccacagggc	ctggcgcacc	ttcgtgctgc	gtgtgcgggc	ccaggaccgc	ccgcctgagc	2220
tgtactttgt	caaggtggat	gtgacggggc	cgtacgacac	catccccag	gacaggtca	2280
cggaggtcat	cgccagcatc	atcaaacccc	agaacacgta	ctgcgtgcgt	cggtatgccg	2340
tgggtccagaa	ggccgcccac	gggcacgtcc	gcaaggcctt	caagagccac	gtctctacct	2400
tgacagacct	ccagccgtac	atgcgacagt	tctggtctca	cctgcaggag	accagccgcg	2460
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tccagtgcc	ggggatccc	cagggctcca	tcctctccac	gctgctctgc	agcctgtgct	2640
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tgggtgatga	tttcttgttg	gtgacacctc	acctcaccca	cgcgaaaacc	ttcctcagga	2760
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acttcctgt	agaagacgag	gccctgggtg	gcacggcttt	tgttcagatg	ccggcccacg	2880
gcctattccc	ctgggtgcggc	ctgctgctgg	ataccgggac	cctggagggtg	cagagcgact	2940
actccaggtg	agcgcacctg	gccggaagtg	gagcctgtgc	ccggctgggg	caggtgctgc	3000
tgcagggccg	ttgcgtccac	ctctgcttcc	gtgtggggca	ggcgactgcc	aatcccaaag	3060
ggtcagatgc	cacaggtgct	ccctcgctcc	atctggggct	gagcacaat	gcatctttct	3120
gtgggagtg	gggtgcctca	caacgggagc	agttttctgt	gctatttttg	taa	3173

&lt;210&gt; 68

<211> 982  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID  
 NO:67 with Intron Y ORF1

<400> 68  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
                   20                  25                  30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
                   35                  40                  45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
                   50                  55                  60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
   65                  70                  75                  80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
                   85                  90                  95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
                   100                  105                  110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
                   115                  120                  125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
   130                  135                  140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
  145                  150                  155                  160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
                   165                  170                  175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
                   180                  185                  190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
                   195                  200                  205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
   210                  215                  220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
  225                  230                  235                  240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
                   245                  250                  255



Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765  
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu  
 785 790 795 800  
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu  
 805 810 815  
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu  
 820 825 830  
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys  
 835 840 845  
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly  
 850 855 860

Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr  
 865 870 875 880  
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu  
 885 890 895  
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr  
 900 905 910  
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr  
 915 920 925  
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu  
 930 935 940  
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly  
 945 950 955 960  
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val  
 965 970 975  
 Gln Ser Asp Tyr Ser Arg  
 980

<210> 69  
 <211> 897  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein 3 (ver.2); encoded by SEQ ID  
 NO:67 with Intron Y ORF2 after the termination  
 codon

<400> 69  
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 Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
 20 25 30  
 Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
 35 40 45  
 Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60  
 Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80  
 Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95  
 Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125  
 Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140  
 Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160  
 Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415

Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460  
 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540  
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp  
 660 665 670  
 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr  
 675 680 685  
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val  
 690 695 700  
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro  
 705 710 715 720

Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg  
                     725                    730                    735  
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser  
                     740                    745                    750  
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg  
                     755                    760                    765  
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser  
                     770                    775                    780  
 Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn  
                     785                    790                    795                    800  
 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val  
                     805                    810                    815  
 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe  
                     820                    825                    830  
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn  
                     835                    840                    845  
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly  
                     850                    855                    860  
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys  
                     865                    870                    875                    880  
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser  
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Arg

<210> 70  
 <211> 982  
 <212> PRT  
 <213> Homo sapiens

<220>  
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       NO:67 with Intron Y ORF3

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 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
                     20                    25                    30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
                     35                    40                    45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

50					55					60					
Pro	Pro	Ala	Ala	Pro	Ser	Phe	Arg	Gln	Val	Pro	Pro	Arg	Gly	Arg	Arg
65					70					75					80
Pro	Ala	Gly	Val	Glu	Gly	Gly	Arg	Gly	Glu	Pro	Ala	Thr	Cys	Gly	Glu
				85					90					95	
Gln	Arg	Arg	Arg	Leu	Arg	Ala	Leu	Pro	Pro	Gln	Val	Ser	Cys	Leu	Lys
			100					105					110		
Glu	Leu	Val	Ala	Arg	Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys
		115					120					125			
Asn	Val	Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly
	130					135					140				
Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr
	145					150					155				160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg
				165					170					175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu
			180					185					190		
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro
		195					200					205			
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
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Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
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Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
			260					265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
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Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
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Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
	305					310					315				320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
			340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser

355	360	365
Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu		
370	375	380
Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu		
385	390	395
Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu		
405	410	415
Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly		
420	425	430
Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro		
435	440	445
Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys		
450	455	460
Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg		
465	470	475
Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr		
485	490	495
Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp		
500	505	510
Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe		
515	520	525
Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp		
530	535	540
Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val		
545	550	555
Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala		
565	570	575
Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg		
580	585	590
Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe		
595	600	605
Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg		
610	615	620
Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val		
625	630	635
Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg		
645	650	655
Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr		

660					665					670					
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	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
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His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
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Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp
			740					745					750		
Thr	Ile	Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys
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Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala
	770					775					780				
Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu
785						790					795				800
Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu
				805					810					815	
Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu
			820					825					830		
Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys
		835					840					845			
His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly
	850					855					860				
Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr
865						870					875				880
Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu
				885					890					895	
Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr
			900					905					910		
His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr
		915					920					925			
Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu
	930					935					940				
Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly
945						950					955				960
Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val

965

970

975

Gln Ser Asp Tyr Ser Arg  
980

&lt;210&gt; 71

&lt;211&gt; 3466

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Altered C-Terminus Protein (ver.2); with Introns  
Y, Alpha, Beta and 3

&lt;400&gt; 71

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<210> 72

<211> 1130

<212> PRT

<213> Homo sapiens

<220>

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ  
ID NO:71 with Intron Y ORF1

<400> 72

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
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Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
65 70 75 80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
85 90 95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
100 105 110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
115 120 125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
130 135 140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
145 150 155 160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
 165 170 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
 180 185 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
 195 200 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
 210 215 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
 225 230 235 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
 245 250 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
 260 265 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
 275 280 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
 290 295 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
 305 310 315 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
 325 330 335  
 His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460

Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765

Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu  
 785 790 795 800  
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu  
 805 810 815  
 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu  
 820 825 830  
 Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys  
 835 840 845  
 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly  
 850 855 860  
 Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr  
 865 870 875 880  
 Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu  
 885 890 895  
 Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr  
 900 905 910  
 His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr  
 915 920 925  
 Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu  
 930 935 940  
 Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly  
 945 950 955 960  
 Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val  
 965 970 975  
 Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu  
 980 985 990  
 Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu  
 995 1000 1005  
 Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln  
 1010 1015 1020  
 Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu  
 1025 1030 1035 1040  
 Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His  
 1045 1050 1055  
 Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp  
 1060 1065 1070

Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu  
 1075 1080 1085

Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro  
 1090 1095 1100

Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val  
 1105 1110 1115 1120

Ser Pro Gly Arg Gly Val Gly Leu Gly Leu  
 1125 1130

<210> 73  
 <211> 1045  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Altered C-Terminus Protein (ver.2); encoded by SEQ  
 ID NO:71 with Intron Y ORF2 after the termination  
 codon

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175

Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
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 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
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 Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480

Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
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 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
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 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
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 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
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 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
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 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile Pro Gln Asp  
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 Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln Asn Thr Tyr  
 675 680 685  
 Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His Gly His Val  
 690 695 700  
 Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp Leu Gln Pro  
 705 710 715 720  
 Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser Pro Leu Arg  
 725 730 735  
 Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu Ala Ser Ser  
 740 745 750  
 Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His Ala Val Arg  
 755 760 765  
 Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro Gln Gly Ser  
 770 775 780

Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp Met Glu Asn  
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 Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu Arg Leu Val  
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 Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala Lys Thr Phe  
 820 825 830  
 Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys Val Val Asn  
 835 840 845  
 Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu Ala Leu Gly  
 850 855 860  
 Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe Pro Trp Cys  
 865 870 875 880  
 Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser Asp Tyr Ser  
 885 890 895  
 Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe Asn Arg Gly  
 900 905 910  
 Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly Val Leu Arg  
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 930 935 940  
 Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln Ala Tyr Arg  
 945 950 955 960  
 Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln Val Trp Lys  
 965 970 975  
 Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala Ser Leu Cys  
 980 985 990  
 Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu Asn Ile Leu Val  
 995 1000 1005  
 Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu Met Glu Pro Pro  
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 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

<223> Altered C-Terminus Protein (ver.2); encoded by SEQ  
ID NO:71 with Intron Y ORF3

&lt;400&gt; 74

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          20          25          30

Pro  Gln  Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
          35          40          45

Ala  Leu  Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
          50          55          60

Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Pro  Pro  Arg  Gly  Arg  Arg
          65          70          75          80

Pro  Ala  Gly  Val  Glu  Gly  Gly  Arg  Gly  Glu  Pro  Ala  Thr  Cys  Gly  Glu
          85          90          95

Gln  Arg  Arg  Arg  Leu  Arg  Ala  Leu  Pro  Pro  Gln  Val  Ser  Cys  Leu  Lys
          100          105          110

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
          115          120          125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
          130          135          140

Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
          145          150          155          160

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
          165          170          175

Arg  Val  Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
          180          185          190

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
          195          200          205

Leu  Tyr  Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
          210          215          220

Ser  Gly  Pro  Arg  Arg  Arg  Leu  Gly  Cys  Glu  Arg  Ala  Trp  Asn  His  Ser
          225          230          235          240

Val  Arg  Glu  Ala  Gly  Val  Pro  Leu  Gly  Leu  Pro  Ala  Pro  Gly  Ala  Arg
          245          250          255

Arg  Arg  Gly  Gly  Ser  Ala  Ser  Arg  Ser  Leu  Pro  Leu  Pro  Lys  Arg  Pro
          260          265          270

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Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys 545	Met	Ser	Val	Arg	Asp 550	Cys	Ala	Trp	Leu	Arg 555	Arg	Ser	Pro	Gly	Val 560
Gly	Cys	Val	Pro	Ala 565	Ala	Glu	His	Arg	Leu 570	Arg	Glu	Glu	Ile	Leu 575	Ala

Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
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 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
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 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp  
 740 745 750  
 Thr Ile Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys  
 755 760 765  
 Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala  
 770 775 780  
 Ala His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu  
 785 790 795 800  
 Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu  
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 Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu  
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 His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly  
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<210> 75
<211> 4022
<212> DNA
<213> Homo sapiens
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<220>  
<223> Protein Lacking Motif A (ver.2); with Introns Y  
and Beta

&lt;400&gt; 75

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ga 4022

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<212> PRT
<213> Homo sapiens

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<220>
<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID
      NO:75 with Intron Y ORF1

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      20              25              30

Pro  Gln Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
      35              40              45

Ala  Leu Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
      50              55              60

Pro  Pro Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Gly  Leu  Pro  Gly  Val  Gly
      65              70              75              80

Val  Arg Leu  Gly  Leu  Arg  Ala  Ala  Gly  Gly  Asn  Gln  Arg  His  Ala  Glu
      85              90              95

Ser  Ser Ala  Gly  Asp  Ser  Gly  Arg  Phe  Pro  Arg  Arg  Ser  Cys  Leu  Lys
      100              105              110

Glu  Leu Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
      115              120              125

Asn  Val Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
      130              135              140

Pro  Pro Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
      145              150              155              160

Val  Thr Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
      165              170              175

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Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205	
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220	
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235	240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	260	265	270	
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	275	280	285	
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	290	295	300	
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	305	310	315	320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	325	330	335	
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Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	355	360	365	
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	370	375	380	
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	385	390	395	400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	405	410	415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	420	425	430	
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	435	440	445	
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	450	455	460	
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg	465	470	475	480

Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala  
 740 745 750  
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val  
 755 760 765  
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His  
 770 775 780

Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	785	790	795	800
His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	805	810	815	
Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	820	825	830	
Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	835	840	845	
Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	850	855	860	
Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	865	870	875	880
Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	885	890	895	
Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	900	905	910	
Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	915	920	925	
Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	930	935	940	
Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	945	950	955	960
Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	Ser	Ser	Tyr	Ala	Arg	Thr	Ser	Ile	965	970	975	
Arg	Ala	Ser	Leu	Thr	Phe	Asn	Arg	Gly	Phe	Lys	Ala	Gly	Arg	Asn	Met	980	985	990	
Arg	Arg	Lys	Leu	Phe	Gly	Val	Leu	Arg	Leu	Lys	Cys	His	Ser	Leu	Phe	995	1000	1005	
Leu	Asp	Leu	Gln	Val	Asn	Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	1010	1015	1020	
Lys	Ile	Leu	Leu	Leu	Gln	Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	1025	1030	1035	1040
Leu	Pro	Phe	His	Gln	Gln	Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	1045	1050	1055	
Val	Ile	Ser	Asp	Thr	Ala	Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	1060	1065	1070	
Asn	Ala	Gly	Met	Ser	Leu	Gly	Ala	Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro	1075	1080	1085	

Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu  
 1090 1095 1100

Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr  
 1105 1110 1115 1120

Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala  
 1125 1130 1135

Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile  
 1140 1145 1150

Leu Asp

<210> 77  
 <211> 1069  
 <212> PRT  
 <213> Homo sapiens

<220>  
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 NO:75 with Intron Y ORF2 after the termination  
 codon

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Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
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Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460

Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val	Gly	Cys	Val	Pro	Ala	465	470	475	480
Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala	Lys	Phe	Leu	His	Trp	485	490	495	
Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe	Phe	Tyr	Val	500	505	510	
Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr	Arg	Lys	Ser	515	520	525	
Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His	Leu	Lys	Arg	530	535	540	
Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln	His	Arg	Glu	545	550	555	560
Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile	Pro	Lys	Pro	565	570	575	
Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val	Gly	Ala	Arg	580	585	590	
Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser	Arg	Val	Lys	595	600	605	
Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg	Pro	Gly	Leu	610	615	620	
Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg	Ala	Trp	Arg	625	630	635	640
Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro	Glu	Leu	Tyr	645	650	655	
Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	660	665	670	
Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala	Ala	675	680	685	
His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr	690	695	700	
Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr	705	710	715	720
Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn	725	730	735	
Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His	740	745	750	
His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile	755	760	765	

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
 770 775 780  
 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu  
 785 790 795 800  
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His  
 805 810 815  
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly  
 820 825 830  
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp  
 835 840 845  
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu  
 850 855 860  
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln  
 865 870 875 880  
 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr  
 885 890 895  
 Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe  
 900 905 910  
 Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val  
 915 920 925  
 Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu  
 930 935 940  
 Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln  
 945 950 955 960  
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr  
 965 970 975  
 Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser  
 980 985 990  
 Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln  
 995 1000 1005  
 Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val  
 1010 1015 1020  
 Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu  
 1025 1030 1035 1040  
 Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala  
 1045 1050 1055  
 Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp  
 1060 1065

<210> 78  
 <211> 1154  
 <212> PRT  
 <213> Homo sapiens

<220>

<223> Protein Lacking Motif A (ver.2); encoded by SEQ ID  
 NO:75 with Intron Y ORF3

<400> 78

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His  Thr  Arg  Glu  Val  Leu  Pro  Leu  Ala  Thr  Phe  Val  Arg  Arg  Leu  Gly
          20              25              30

Pro  Gln  Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
          35              40              45

Ala  Leu  Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
          50              55              60

Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Pro  Pro  Arg  Gly  Arg  Arg
65              70              75              80

Pro  Ala  Gly  Val  Glu  Gly  Gly  Arg  Gly  Glu  Pro  Ala  Thr  Cys  Gly  Glu
          85              90              95

Gln  Arg  Arg  Arg  Leu  Arg  Ala  Leu  Pro  Gln  Val  Ser  Cys  Leu  Lys
          100             105             110

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
          115             120             125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
          130             135             140

Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
145              150              155              160

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
          165              170              175

Arg  Val  Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
          180             185             190

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
          195              200              205

Leu  Tyr  Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
          210              215              220

Ser  Gly  Pro  Arg  Arg  Arg  Leu  Gly  Cys  Glu  Arg  Ala  Trp  Asn  His  Ser
225              230              235              240

Val  Arg  Glu  Ala  Gly  Val  Pro  Leu  Gly  Leu  Pro  Ala  Pro  Gly  Ala  Arg

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			245					250					255		
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Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
Gly	Ser	Arg	Pro	Trp 405	Met	Pro	Gly	Thr	Pro 410	Arg	Arg	Leu	Pro	Arg 415	Leu
Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
Asn	His	Ala 435	Gln	Cys	Pro	Tyr	Gly 440	Val	Leu	Leu	Lys	Thr 445	His	Cys	Pro
Leu	Arg 450	Ala	Ala	Val	Thr	Pro 455	Ala	Ala	Gly	Val	Cys 460	Ala	Arg	Glu	Lys
Pro 465	Gln	Gly	Ser	Val	Ala 470	Ala	Pro	Glu	Glu	Glu 475	Asp	Thr	Asp	Pro	Arg 480
Arg	Leu	Val	Gln	Leu 485	Leu	Arg	Gln	His	Ser 490	Ser	Pro	Trp	Gln	Val 495	Tyr
Gly	Phe	Val	Arg 500	Ala	Cys	Leu	Arg	Arg 505	Leu	Val	Pro	Pro	Gly 510	Leu	Trp
Gly	Ser	Arg 515	His	Asn	Glu	Arg	Arg 520	Phe	Leu	Arg	Asn	Thr 525	Lys	Lys	Phe
Ile	Ser 530	Leu	Gly	Lys	His	Ala 535	Lys	Leu	Ser	Leu	Gln 540	Glu	Leu	Thr	Trp
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val

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Gly Cys Val Pro	Ala Ala Glu His Arg	Leu Arg Glu Glu Ile Leu Ala				
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Lys Phe Leu His Trp	Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg					
	580	585			590	
Ser Phe Phe Tyr Val Thr	Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe					
	595	600			605	
Phe Tyr Arg Lys Ser Val Trp	Ser Lys Leu Gln Ser Ile Gly Ile Arg					
	610	615			620	
Gln His Leu Lys Arg Val Gln	Leu Arg Glu Leu Ser Glu Ala Glu Val					
	625	630			635	640
Arg Gln His Arg Glu Ala Arg	Pro Ala Leu Leu Thr Ser Arg Leu Arg					
	645	650			655	
Phe Ile Pro Lys Pro Asp Gly	Leu Arg Pro Ile Val Asn Met Asp Tyr					
	660	665			670	
Val Val Gly Ala Arg Thr Phe	Arg Arg Glu Lys Arg Ala Glu Arg Leu					
	675	680			685	
Thr Ser Arg Val Lys Ala Leu	Phe Ser Val Leu Asn Tyr Glu Arg Ala					
	690	695			700	
Arg Arg Pro Gly Leu Leu Gly	Ala Ser Val Leu Gly Leu Asp Asp Ile					
	705	710			715	720
His Arg Ala Trp Arg Thr Phe	Val Leu Arg Val Arg Ala Gln Asp Pro					
	725	730			735	
Pro Pro Glu Leu Tyr Phe Val	Lys Asp Arg Leu Thr Glu Val Ile Ala					
	740	745			750	
Ser Ile Ile Lys Pro Gln Asn	Thr Tyr Cys Val Arg Arg Tyr Ala Val					
	755	760			765	
Val Gln Lys Ala Ala His Gly	His Val Arg Lys Ala Phe Lys Ser His					
	770	775			780	
Val Ser Thr Leu Thr Asp Leu	Gln Pro Tyr Met Arg Gln Phe Val Ala					
	785	790			795	800
His Leu Gln Glu Thr Ser Pro	Leu Arg Asp Ala Val Val Ile Glu Gln					
	805	810			815	
Ser Ser Ser Leu Asn Glu Ala	Ser Ser Gly Leu Phe Asp Val Phe Leu					
	820	825			830	
Arg Phe Met Cys His His Ala	Val Arg Ile Arg Gly Lys Ser Tyr Val					
	835	840			845	
Gln Cys Gln Gly Ile Pro Gln	Gly Ser Ile Leu Ser Thr Leu Leu Cys					

850	855	860
Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg 865 870 875 880		
Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr 885 890 895		
Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly 900 905 910		
Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn 915 920 925		
Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met 930 935 940		
Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg 945 950 955 960		
Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile 965 970 975		
Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met 980 985 990		
Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe 995 1000 1005		
Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr 1010 1015 1020		
Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln 1025 1030 1035 1040		
Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg 1045 1050 1055		
Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys 1060 1065 1070		
Asn Ala Gly Met Ser Leu Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro 1075 1080 1085		
Ser Glu Ala Val Gln Trp Leu Cys His Gln Ala Phe Leu Leu Lys Leu 1090 1095 1100		
Thr Arg His Arg Val Thr Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr 1105 1110 1115 1120		
Ala Gln Thr Gln Leu Ser Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala 1125 1130 1135		
Leu Glu Ala Ala Ala Asn Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile 1140 1145 1150		
Leu Asp		

<210> 79  
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 <212> DNA  
 <213> Homo sapiens

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 Introns Y, Beta and 2

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 gcagagaaa gagggccgag cgtctcacct cgaggggtga ggcactgttc agcgtgtca 2100  
 actacagcg ggccgcgcgc cccggcctcc tgggcgcctc tgtgtggggc ctggacgata 2160  
 tccacagggc ctggcgacc ttcgtgctgc gtgtgcgggc ccaggaccgc ccgctgagc 2220  
 tgtactttgt caaggacagg ctacagggag tcatcgccag catcatcaa cccagaaca 2280  
 cgtactgct gcgtcggtat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340  
 ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400  
 ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460  
 tgaatgaggc cagcagtggc ctcttcgacg tcttctacg cttcatgtgc caccacgccg 2520  
 tgcgcacag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580  
 ccacgtgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640

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ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
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tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
cttttgttca gatgccggcc cacggcctat tcccctggtg cggcctgctg ctggataccc 2880
ggaccctgga ggtgcagagc gactactcca ggtgagcgca cctggccgga agtggagcct 2940
gtgcccggct ggggcaggtg ctgctgcagg gccgttgctg ccacctctgc ttccgtgtgg 3000
ggcaggcgac tgccaatccc aaagggtcag atgccacagg gtgcccctcg tcccatctgg 3060
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<210> 80
<211> 970
<212> PRT
<213> Homo sapiens

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<220>
<223> Truncated Protein lacking Motif A (ver.2); encoded
      by SEQ ID NO:79 with Intron Y ORF1

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His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
      20              25              30

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
      35              40              45

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
      50              55              60

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly
      65              70              75              80

Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu
      85              90              95

Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys
      100             105             110

Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys
      115             120             125

Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly
      130             135             140

Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr
      145             150             155             160

Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg
      165             170             175

Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu
      180             185             190

Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro

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195					200					205					
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala
210					215					220					
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser
225					230					235					240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg
				245					250					255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro
			260					265					270		
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly
			275				280					285			
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe
	290					295					300				
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu
305					310					315					320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln
				325					330					335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp
			340					345					350		
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser
		355					360					365			
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu
	370					375					380				
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu
385					390					395					400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu
				405					410					415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly
			420					425					430		
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro
		435					440					445			
Leu	Arg	Ala	Ala	Val	Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys
	450					455					460				
Pro	Gln	Gly	Ser	Val	Ala	Ala	Pro	Glu	Glu	Glu	Asp	Thr	Asp	Pro	Arg
465					470					475					480
Arg	Leu	Val	Gln	Leu	Leu	Arg	Gln	His	Ser	Ser	Pro	Trp	Gln	Val	Tyr
				485					490					495	
Gly	Phe	Val	Arg	Ala	Cys	Leu	Arg	Arg	Leu	Val	Pro	Pro	Gly	Leu	Trp

500					505					510					
Gly	Ser	Arg	His	Asn	Glu	Arg	Arg	Phe	Leu	Arg	Asn	Thr	Lys	Lys	Phe
		515					520					525			
Ile	Ser	Leu	Gly	Lys	His	Ala	Lys	Leu	Ser	Leu	Gln	Glu	Leu	Thr	Trp
	530					535					540				
Lys	Met	Ser	Val	Arg	Asp	Cys	Ala	Trp	Leu	Arg	Arg	Ser	Pro	Gly	Val
545					550					555					560
Gly	Cys	Val	Pro	Ala	Ala	Glu	His	Arg	Leu	Arg	Glu	Glu	Ile	Leu	Ala
				565					570					575	
Lys	Phe	Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg
			580					585					590		
Ser	Phe	Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe
		595					600					605			
Phe	Tyr	Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg
	610					615					620				
Gln	His	Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val
625					630					635					640
Arg	Gln	His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg
				645					650					655	
Phe	Ile	Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr
			660					665					670		
Val	Val	Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu
		675					680					685			
Thr	Ser	Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala
	690					695					700				
Arg	Arg	Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile
705					710					715					720
His	Arg	Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro
				725					730					735	
Pro	Pro	Glu	Leu	Tyr	Phe	Val	Lys	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala
			740					745					750		
Ser	Ile	Ile	Lys	Pro	Gln	Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val
		755					760					765			
Val	Gln	Lys	Ala	Ala	His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His
	770					775					780				
Val	Ser	Thr	Leu	Thr	Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala
785					790					795					800
His	Leu	Gln	Glu	Thr	Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln

805					810					815					
Ser	Ser	Ser	Leu	Asn	Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu
			820					825					830		
Arg	Phe	Met	Cys	His	His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val
		835					840					845			
Gln	Cys	Gln	Gly	Ile	Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys
	850					855					860				
Ser	Leu	Cys	Tyr	Gly	Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg
865					870					875					880
Arg	Asp	Gly	Leu	Leu	Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr
			885						890					895	
Pro	His	Leu	Thr	His	Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly
		900						905					910		
Val	Pro	Glu	Tyr	Gly	Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn
		915					920					925			
Phe	Pro	Val	Glu	Asp	Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met
	930					935					940				
Pro	Ala	His	Gly	Leu	Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg
945					950					955					960
Thr	Leu	Glu	Val	Gln	Ser	Asp	Tyr	Ser	Arg						
			965						970						

<210> 81  
 <211> 885  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Truncated Protein lacking Motif A (ver.2); encoded  
 by SEQ ID NO:79 with Intron Y ORF2 after the  
 termination codon

<400> 81															
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Gln	Gly	Ala	Ser	Pro	Ala	Gly	Ser	Cys	Leu	Lys	Glu	Leu	Val	Ala	Arg
			20					25					30		
Val	Leu	Gln	Arg	Leu	Cys	Glu	Arg	Gly	Ala	Lys	Asn	Val	Leu	Ala	Phe
		35					40					45			
Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro	Glu	Ala	Phe
	50					55					60				
Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr	Asp	Ala	Leu

65					70						75				80
Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val	Gly	Asp	Asp
				85					90					95	
Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val	Leu	Val	Ala
			100					105					110		
Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr	Gln	Leu	Gly
		115					120					125			
Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly	Pro	Arg	Arg
		130				135					140				
Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg	Glu	Ala	Gly
145					150					155					160
Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg	Gly	Gly	Ser
				165					170					175	
Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg	Gly	Ala	Ala
			180					185					190		
Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp	Ala	His	Pro
		195					200					205			
Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val	Val	Ser	Pro
	210					215					220				
Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala	Leu	Ser	Gly
225					230					235					240
Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His	Ala	Gly	Pro
				245					250					255	
Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro	Cys	Pro	Pro
			260					265					270		
Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	Ser	Gly	Asp	Lys	Glu
		275					280					285			
Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	Arg	Pro	Ser	Leu	Thr
	290					295					300				
Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	Gly	Ser	Arg	Pro	Trp
305					310					315					320
Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	Pro	Gln	Arg	Tyr	Trp
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Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	Asn	His	Ala	Gln	Cys
			340					345					350		
Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	Leu	Arg	Ala	Ala	Val
		355					360					365			
Thr	Pro	Ala	Ala	Gly	Val	Cys	Ala	Arg	Glu	Lys	Pro	Gln	Gly	Ser	Val

370	375	380
Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu 385 390 395 400		
Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala 405 410 415		
Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn 420 425 430		
Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys 435 440 445		
His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg 450 455 460		
Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala 465 470 475 480		
Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp 485 490 495		
Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val 500 505 510		
Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser 515 520 525		
Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg 530 535 540		
Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu 545 550 555 560		
Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro 565 570 575		
Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg 580 585 590		
Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys 595 600 605		
Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu 610 615 620		
Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg 625 630 635 640		
Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr 645 650 655		
Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro 660 665 670		
Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala		

675					680					685					
His	Gly	His	Val	Arg	Lys	Ala	Phe	Lys	Ser	His	Val	Ser	Thr	Leu	Thr
690						695					700				
Asp	Leu	Gln	Pro	Tyr	Met	Arg	Gln	Phe	Val	Ala	His	Leu	Gln	Glu	Thr
705					710					715					720
Ser	Pro	Leu	Arg	Asp	Ala	Val	Val	Ile	Glu	Gln	Ser	Ser	Ser	Leu	Asn
				725					730					735	
Glu	Ala	Ser	Ser	Gly	Leu	Phe	Asp	Val	Phe	Leu	Arg	Phe	Met	Cys	His
				740				745					750		
His	Ala	Val	Arg	Ile	Arg	Gly	Lys	Ser	Tyr	Val	Gln	Cys	Gln	Gly	Ile
		755					760					765			
Pro	Gln	Gly	Ser	Ile	Leu	Ser	Thr	Leu	Leu	Cys	Ser	Leu	Cys	Tyr	Gly
	770					775					780				
Asp	Met	Glu	Asn	Lys	Leu	Phe	Ala	Gly	Ile	Arg	Arg	Asp	Gly	Leu	Leu
785					790					795					800
Leu	Arg	Leu	Val	Asp	Asp	Phe	Leu	Leu	Val	Thr	Pro	His	Leu	Thr	His
				805					810					815	
Ala	Lys	Thr	Phe	Leu	Arg	Thr	Leu	Val	Arg	Gly	Val	Pro	Glu	Tyr	Gly
			820					825					830		
Cys	Val	Val	Asn	Leu	Arg	Lys	Thr	Val	Val	Asn	Phe	Pro	Val	Glu	Asp
	835					840					845				
Glu	Ala	Leu	Gly	Gly	Thr	Ala	Phe	Val	Gln	Met	Pro	Ala	His	Gly	Leu
	850					855					860				
Phe	Pro	Trp	Cys	Gly	Leu	Leu	Leu	Asp	Thr	Arg	Thr	Leu	Glu	Val	Gln
865					870					875					880
Ser	Asp	Tyr	Ser	Arg											
				885											

&lt;210&gt; 82

&lt;211&gt; 970

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

<223> Truncated Protein lacking Motif A (ver.2); encoded  
by SEQ ID NO:79 with Intron Y ORF3

&lt;400&gt; 82

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His	Thr	Arg	Glu	Val	Leu	Pro	Leu	Ala	Thr	Phe	Val	Arg	Arg	Leu	Gly
			20					25					30		

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
                   35                                  40                                  45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
           50                                  55                                  60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
   65                                  70                                  75                                  80  
 Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
                   85                                  90                                  95  
 Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
                  100                                 105                                 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
          115                                 120                                 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
   130                                 135                                 140  
 Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
  145                                 150                                 155                                 160  
 Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg  
                  165                                 170                                 175  
 Arg Val Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu  
                  180                                 185                                 190  
 Phe Val Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro  
   195                                 200                                 205  
 Leu Tyr Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala  
   210                                 215                                 220  
 Ser Gly Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser  
  225                                 230                                 235                                 240  
 Val Arg Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg  
                  245                                 250                                 255  
 Arg Arg Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro  
                  260                                 265                                 270  
 Arg Arg Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly  
   275                                 280                                 285  
 Ser Trp Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe  
   290                                 295                                 300  
 Cys Val Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu  
  305                                 310                                 315                                 320  
 Gly Ala Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln  
                  325                                 330                                 335

His His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp  
 340 345 350  
 Thr Pro Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser  
 355 360 365  
 Ser Gly Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu  
 370 375 380  
 Arg Pro Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu  
 385 390 395 400  
 Gly Ser Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu  
 405 410 415  
 Pro Gln Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly  
 420 425 430  
 Asn His Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro  
 435 440 445  
 Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640

Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala  
 740 745 750  
 Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val  
 755 760 765  
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His  
 770 775 780  
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala  
 785 790 795 800  
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln  
 805 810 815  
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu  
 820 825 830  
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val  
 835 840 845  
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys  
 850 855 860  
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg  
 865 870 875 880  
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr  
 885 890 895  
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly  
 900 905 910  
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn  
 915 920 925  
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met  
 930 935 940

Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg  
 945 950 955 960

Thr Leu Glu Val Gln Ser Asp Tyr Ser Arg  
 965 970

<210> 83  
 <211> 3432  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus  
 (ver.2); with Intron Y, Beta and 3

<400> 83  
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 cgcggggacc cggcggtttt ccgcgcgctg gtggcccagt gcctggtgtg cgtgccctgg 180  
 gacgcacggc cggccccgcg cggccccctc ttccgccagg tgggcctccc cggggctcggc 240  
 gtccggctgg ggttgagggc ggccgggggg aaccagcgac atgcggagag cagcgcaggc 300  
 gactcagggc gcttcccccg caggtgtcct gcctgaagga gctggtggcc cgagtgtgc 360  
 agaggctgtg cgagcgcggc gcgaagaacg tgctggcctt cggcttcgcg ctgctggacg 420  
 gggcccgcg gggccccccc gaggccttca ccaccagcgt gcgcagctac ctgccccaca 480  
 cgggtgaccga cgcactgcgg gggagcgggg cgtgggggct gctgctgcgc cgcgtgggcg 540  
 acgacgtgct ggttcacctg ctggcacgct gcgcgctctt tgtgctggtg gctcccagct 600  
 gcgcctacca ggtgtgcggg ccgcgcgctg accagctcgg cgtgccact caggccccgc 660  
 ccccgccaca cgctagtga ccccgaaagg gtctgggatg cgaacggggc tggaaaccata 720  
 gcgtcagga ggcgggggtc cccctgggac tgcagcccc ggtgcgagg aggcgcgggg 780  
 gcagtgcag ccgaagtctg ccgttgccca agaggccag gcgtggcgct gccctgagc 840  
 cggagcggac gcccgttggg caggggtcct gggccaccc gggcaggacg cgtggaccga 900  
 gtgaccgtgg tttctgtgtg gtgtcacctg ccagaccgc cgaagaagcc acctctttgg 960  
 aggggtgcgt ctctggcacg cgcactccc acccatccgt gggccgccag caccacgcgg 1020  
 gcccccatc cacatcgcg ccaccacgtc cctgggacac gccttgtccc ccggtgtacg 1080  
 ccgagacca gcaattcctc tactcctcag gcgacaagga gcagctgcgg cctccttcc 1140  
 tactcagctc tctgaggccc agcctgactg gcgctcggag gctcgtggag accatctttc 1200  
 tgggttccag gccctggatg ccagggactc cccgcagggt gccccgcctg cccagcgct 1260  
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 gtgcccggga gaagccccag ggctctgtgg cggcccccga ggaggaggac acagaccccc 1440  
 gtcgcctggt gcagctgtc cgccagcaca gcagccccg gcaggtgtac ggcttcgtgc 1500  
 gggcctgcct gcgcccgtg gtgccccag gcctctgggg ctccaggcac aacgaacgcc 1560  
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 aggagctgac gtggaagatg agcgtgcggg actgcgctt gctgcgcagg agcccagggg 1680  
 ttggtgtgt tccggccgca gagcaccgtc tgctgagga gatcctggcc aagttcctgc 1740  
 actggtgat gagtgttac gtcgtcgagc tgctcaggtc tttcttttat gtcacggaga 1800  
 ccacgtttca aaagaacagg ctcttttct accggaagag tgtctggagc aagttgcaaa 1860  
 gcattggaat cagacagcac ttgaagagg tgacgtgcg ggagctgtcg gaagcagagg 1920  
 tcaggcagca tcgggaagcc aggccgccc tgctgacgtc cagactccgc ttcaccccca 1980  
 agcctgacgg gctgcggccg attgtgaaca tggactacgt cgtgggagcc agaacgttcc 2040  
 gcagagaaaa gagggccgag cgtctcacct cgagggtgaa ggcactgttc agcgtgctca 2100  
 actacgagcg ggcgcgcgcc cccggcctcc tgggcgcctc tgtgctgggc ctggacgata 2160  
 tccacagggc ctggcgaccc ttcgtgctgc gtgtgcgggc ccaggacccg ccgcctgagc 2220  
 tgtactttgt caaggacagg ctcacggagg tcatcgccag catcatcaaa cccagaaca 2280  
 cgtactgcgt gcgtcggat gccgtggtcc agaaggccgc ccatgggcac gtccgcaagg 2340

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ccttcaagag ccacgtctct accttgacag acctccagcc gtacatgcga cagttcgtgg 2400
ctcacctgca ggagaccagc ccgctgaggg atgccgtcgt catcgagcag agctcctccc 2460
tgaatgaggg cagcagtggc ctcttcgacg tcttcctacg cttcatgtgc caccacgccg 2520
tgcgcatcag gggcaagtcc tacgtccagt gccaggggat cccgcagggc tccatcctct 2580
ccacgctgct ctgcagcctg tgctacggcg acatggagaa caagctgttt gcggggattc 2640
ggcgggacgg gctgctcctg cgtttggtgg atgatttctt gttggtgaca cctcacctca 2700
cccacgcgaa aaccttcctc aggaccctgg tccgaggtgt ccctgagtat ggctgcgtgg 2760
tgaacttgcg gaagacagtg gtgaacttcc ctgtagaaga cgaggccctg ggtggcacgg 2820
cttttgttca gatgccggcc cacggcctat tcccctggtg cggcctgctg ctggataccc 2880
ggaccctgga ggtgcagagc gactactcca gctatgcccg gacctccatc agagccagtc 2940
tcaccttcaa ccgcggcttc aaggctggga ggaacatgcg tcgcaaactc tttggggctc 3000
tgcggtgtaa gtgtcacagc ctgtttctgg atttgcaggt gaacagcctc cagacggtgt 3060
gcaccaacat ctacaagatc ctctgctgc aggcgtacag gtttcacgca tgtgtgctgc 3120
agctcccat tcatcagcaa gtttggaaga accccacatt tttcctgcgc gtcatctctg 3180
acacggcctc cctctgctac tccatcctga aagccaagaa cgcagccgaa gaaaacattt 3240
ctgtcgtgac tctgcggtg cttgggtcgg gacagccaga gatggagcca cccgcagac 3300
cgtcgggtgt gggcagcttt ccggtgtctc ctgggagggg agttgggctg ggcctgtgac 3360
tcctcagcct ctgttttccc ccagggatgt cgctgggggc caagggcgcc gccggccctc 3420
tgccctccga ga 3432

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<210> 84  
 <211> 1122  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus  
 (ver.2); encoded by SEQ ID NO:83 with Intron Y  
 ORF1

<400> 84  
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
 1 5 10 15  
 His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
 20 25 30  
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
 35 40 45  
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
 50 55 60  
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Gly Leu Pro Gly Val Gly  
 65 70 75 80  
 Val Arg Leu Gly Leu Arg Ala Ala Gly Gly Asn Gln Arg His Ala Glu  
 85 90 95  
 Ser Ser Ala Gly Asp Ser Gly Arg Phe Pro Arg Arg Ser Cys Leu Lys  
 100 105 110  
 Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
 115 120 125  
 Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
 130 135 140

Pro	Pro	Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	145	150	155	160
Val	Thr	Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	165	170	175	
Arg	Val	Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	180	185	190	
Phe	Val	Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	195	200	205	
Leu	Tyr	Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	210	215	220	
Ser	Gly	Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	225	230	235	240
Val	Arg	Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	245	250	255	
Arg	Arg	Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	260	265	270	
Arg	Arg	Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	275	280	285	
Ser	Trp	Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	290	295	300	
Cys	Val	Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	305	310	315	320
Gly	Ala	Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	325	330	335	
His	His	Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	340	345	350	
Thr	Pro	Cys	Pro	Pro	Val	Tyr	Ala	Glu	Thr	Lys	His	Phe	Leu	Tyr	Ser	355	360	365	
Ser	Gly	Asp	Lys	Glu	Gln	Leu	Arg	Pro	Ser	Phe	Leu	Leu	Ser	Ser	Leu	370	375	380	
Arg	Pro	Ser	Leu	Thr	Gly	Ala	Arg	Arg	Leu	Val	Glu	Thr	Ile	Phe	Leu	385	390	395	400
Gly	Ser	Arg	Pro	Trp	Met	Pro	Gly	Thr	Pro	Arg	Arg	Leu	Pro	Arg	Leu	405	410	415	
Pro	Gln	Arg	Tyr	Trp	Gln	Met	Arg	Pro	Leu	Phe	Leu	Glu	Leu	Leu	Gly	420	425	430	
Asn	His	Ala	Gln	Cys	Pro	Tyr	Gly	Val	Leu	Leu	Lys	Thr	His	Cys	Pro	435	440	445	

Leu Arg Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys  
 450 455 460  
 Pro Gln Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg  
 465 470 475 480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
 485 490 495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
 500 505 510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
 515 520 525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
 530 535 540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
 545 550 555 560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
 565 570 575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
 580 585 590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
 595 600 605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg  
 610 615 620  
 Gln His Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val  
 625 630 635 640  
 Arg Gln His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg  
 645 650 655  
 Phe Ile Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr  
 660 665 670  
 Val Val Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu  
 675 680 685  
 Thr Ser Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala  
 690 695 700  
 Arg Arg Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile  
 705 710 715 720  
 His Arg Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro  
 725 730 735  
 Pro Pro Glu Leu Tyr Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala  
 740 745 750

Ser Ile Ile Lys Pro Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val  
 755 760 765  
 Val Gln Lys Ala Ala His Gly His Val Arg Lys Ala Phe Lys Ser His  
 770 775 780  
 Val Ser Thr Leu Thr Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala  
 785 790 795 800  
 His Leu Gln Glu Thr Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln  
 805 810 815  
 Ser Ser Ser Leu Asn Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu  
 820 825 830  
 Arg Phe Met Cys His His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val  
 835 840 845  
 Gln Cys Gln Gly Ile Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys  
 850 855 860  
 Ser Leu Cys Tyr Gly Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg  
 865 870 875 880  
 Arg Asp Gly Leu Leu Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr  
 885 890 895  
 Pro His Leu Thr His Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly  
 900 905 910  
 Val Pro Glu Tyr Gly Cys Val Val Asn Leu Arg Lys Thr Val Val Asn  
 915 920 925  
 Phe Pro Val Glu Asp Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met  
 930 935 940  
 Pro Ala His Gly Leu Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg  
 945 950 955 960  
 Thr Leu Glu Val Gln Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile  
 965 970 975  
 Arg Ala Ser Leu Thr Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met  
 980 985 990  
 Arg Arg Lys Leu Phe Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe  
 995 1000 1005  
 Leu Asp Leu Gln Val Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr  
 1010 1015 1020  
 Lys Ile Leu Leu Leu Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln  
 1025 1030 1035 1040  
 Leu Pro Phe His Gln Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg  
 1045 1050 1055

Val Ile Ser Asp Thr Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys  
 1060 1065 1070

Asn Ala Glu Glu Glu Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly  
 1075 1080 1085

Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly  
 1090 1095 1100

Ser Phe Pro Val Ser Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile  
 1105 1110 1115 1120

Gly Ala

<210> 85  
 <211> 1037  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> Protein Lacking Motif A and Altered C-Terminus  
 (ver.2); encoded by SEQ ID NO:83 with Intron Y  
 ORF2 after the termination codon

<400> 85  
 Gly Arg Pro Gly Gly Thr Ser Asp Met Arg Arg Ala Ala Gln Ala Thr  
 1 5 10 15

Gln Gly Ala Ser Pro Ala Gly Ser Cys Leu Lys Glu Leu Val Ala Arg  
 20 25 30

Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val Leu Ala Phe  
 35 40 45

Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro Glu Ala Phe  
 50 55 60

Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr Asp Ala Leu  
 65 70 75 80

Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val Gly Asp Asp  
 85 90 95

Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val Leu Val Ala  
 100 105 110

Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr Gln Leu Gly  
 115 120 125

Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly Pro Arg Arg  
 130 135 140

Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg Glu Ala Gly  
 145 150 155 160

Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg Gly Gly Ser  
 165 170 175  
 Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg Gly Ala Ala  
 180 185 190  
 Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp Ala His Pro  
 195 200 205  
 Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val Val Ser Pro  
 210 215 220  
 Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala Leu Ser Gly  
 225 230 235 240  
 Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His Ala Gly Pro  
 245 250 255  
 Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro Cys Pro Pro  
 260 265 270  
 Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly Asp Lys Glu  
 275 280 285  
 Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro Ser Leu Thr  
 290 295 300  
 Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser Arg Pro Trp  
 305 310 315 320  
 Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln Arg Tyr Trp  
 325 330 335  
 Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His Ala Gln Cys  
 340 345 350  
 Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg Ala Ala Val  
 355 360 365  
 Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln Gly Ser Val  
 370 375 380  
 Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu Val Gln Leu  
 385 390 395 400  
 Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe Val Arg Ala  
 405 410 415  
 Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser Arg His Asn  
 420 425 430  
 Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser Leu Gly Lys  
 435 440 445  
 His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met Ser Val Arg  
 450 455 460

Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys Val Pro Ala  
 465 470 475 480  
 Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe Leu His Trp  
 485 490 495  
 Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe Phe Tyr Val  
 500 505 510  
 Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr Arg Lys Ser  
 515 520 525  
 Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His Leu Lys Arg  
 530 535 540  
 Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln His Arg Glu  
 545 550 555 560  
 Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile Pro Lys Pro  
 565 570 575  
 Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val Gly Ala Arg  
 580 585 590  
 Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser Arg Val Lys  
 595 600 605  
 Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg Pro Gly Leu  
 610 615 620  
 Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg Ala Trp Arg  
 625 630 635 640  
 Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro Glu Leu Tyr  
 645 650 655  
 Phe Val Lys Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro  
 660 665 670  
 Gln Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala  
 675 680 685  
 His Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr  
 690 695 700  
 Asp Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr  
 705 710 715 720  
 Ser Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn  
 725 730 735  
 Glu Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His  
 740 745 750  
 His Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile  
 755 760 765

Pro Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly  
 770 775 780  
 Asp Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu  
 785 790 795 800  
 Leu Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His  
 805 810 815  
 Ala Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly  
 820 825 830  
 Cys Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp  
 835 840 845  
 Glu Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu  
 850 855 860  
 Phe Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln  
 865 870 875 880  
 Ser Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr  
 885 890 895  
 Phe Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe  
 900 905 910  
 Gly Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val  
 915 920 925  
 Asn Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu  
 930 935 940  
 Gln Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln  
 945 950 955 960  
 Gln Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr  
 965 970 975  
 Ala Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Glu Glu Glu  
 980 985 990  
 Asn Ile Leu Val Val Thr Pro Ala Val Leu Gly Ser Gly Gln Pro Glu  
 995 1000 1005  
 Met Glu Pro Pro Arg Arg Pro Ser Gly Val Gly Ser Phe Pro Val Ser  
 1010 1015 1020  
 Pro Gly Arg Gly Val Gly Leu Gly Leu Phe Ile Gly Ala  
 1025 1030 1035

<210> 86  
 <211> 1122  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

<223> Protein Lacking Motif A and Altered C-Terminus  
 (ver.2); encoded by SEQ ID NO:83 with Intron Y  
 ORF3

&lt;400&gt; 86

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Met  Pro  Arg  Ala  Pro  Arg  Cys  Arg  Ala  Val  Arg  Ser  Leu  Leu  Arg  Ser
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His  Thr  Arg  Glu  Val  Leu  Pro  Leu  Ala  Thr  Phe  Val  Arg  Arg  Leu  Gly
          20          25          30

Pro  Gln  Gly  Trp  Arg  Leu  Val  Gln  Arg  Gly  Asp  Pro  Ala  Ala  Phe  Arg
          35          40          45

Ala  Leu  Val  Ala  Gln  Cys  Leu  Val  Cys  Val  Pro  Trp  Asp  Ala  Arg  Pro
 50          55          60

Pro  Pro  Ala  Ala  Pro  Ser  Phe  Arg  Gln  Val  Pro  Pro  Arg  Gly  Arg  Arg
 65          70          75          80

Pro  Ala  Gly  Val  Glu  Gly  Gly  Arg  Gly  Glu  Pro  Ala  Thr  Cys  Gly  Glu
          85          90          95

Gln  Arg  Arg  Arg  Leu  Arg  Ala  Leu  Pro  Pro  Gln  Val  Ser  Cys  Leu  Lys
          100          105          110

Glu  Leu  Val  Ala  Arg  Val  Leu  Gln  Arg  Leu  Cys  Glu  Arg  Gly  Ala  Lys
          115          120          125

Asn  Val  Leu  Ala  Phe  Gly  Phe  Ala  Leu  Leu  Asp  Gly  Ala  Arg  Gly  Gly
          130          135          140

Pro  Pro  Glu  Ala  Phe  Thr  Thr  Ser  Val  Arg  Ser  Tyr  Leu  Pro  Asn  Thr
          145          150          155          160

Val  Thr  Asp  Ala  Leu  Arg  Gly  Ser  Gly  Ala  Trp  Gly  Leu  Leu  Leu  Arg
          165          170          175

Arg  Val  Gly  Asp  Asp  Val  Leu  Val  His  Leu  Leu  Ala  Arg  Cys  Ala  Leu
          180          185          190

Phe  Val  Leu  Val  Ala  Pro  Ser  Cys  Ala  Tyr  Gln  Val  Cys  Gly  Pro  Pro
          195          200          205

Leu  Tyr  Gln  Leu  Gly  Ala  Ala  Thr  Gln  Ala  Arg  Pro  Pro  Pro  His  Ala
          210          215          220

Ser  Gly  Pro  Arg  Arg  Arg  Leu  Gly  Cys  Glu  Arg  Ala  Trp  Asn  His  Ser
          225          230          235          240

Val  Arg  Glu  Ala  Gly  Val  Pro  Leu  Gly  Leu  Pro  Ala  Pro  Gly  Ala  Arg
          245          250          255

Arg  Arg  Gly  Gly  Ser  Ala  Ser  Arg  Ser  Leu  Pro  Leu  Pro  Lys  Arg  Pro
          260          265          270

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Arg	Arg	Gly 275	Ala	Ala	Pro	Glu	Pro 280	Glu	Arg	Thr	Pro	Val 285	Gly	Gln	Gly
Ser	Trp 290	Ala	His	Pro	Gly	Arg 295	Thr	Arg	Gly	Pro	Ser 300	Asp	Arg	Gly	Phe
Cys 305	Val	Val	Ser	Pro	Ala 310	Arg	Pro	Ala	Glu	Glu 315	Ala	Thr	Ser	Leu	Glu 320
Gly	Ala	Leu	Ser	Gly 325	Thr	Arg	His	Ser	His 330	Pro	Ser	Val	Gly	Arg 335	Gln
His	His	Ala	Gly 340	Pro	Pro	Ser	Thr	Ser 345	Arg	Pro	Pro	Arg	Pro 350	Trp	Asp
Thr	Pro	Cys 355	Pro	Pro	Val	Tyr	Ala 360	Glu	Thr	Lys	His	Phe 365	Leu	Tyr	Ser
Ser	Gly 370	Asp	Lys	Glu	Gln	Leu 375	Arg	Pro	Ser	Phe	Leu 380	Leu	Ser	Ser	Leu
Arg 385	Pro	Ser	Leu	Thr	Gly 390	Ala	Arg	Arg	Leu	Val 395	Glu	Thr	Ile	Phe	Leu 400
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Pro	Gln	Arg	Tyr 420	Trp	Gln	Met	Arg	Pro 425	Leu	Phe	Leu	Glu	Leu 430	Leu	Gly
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&lt;223&gt; Human Telomerase Clone with Exon Beta Spliced Out

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actctttggg gtcttgccgc tgaagtgtca cagcctgttt ctggatttgc aggtgaacag 7260
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atctagag

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<210> 90
<211> 8
<212> PRT
<213> Homo sapiens

```

```

<400> 90
Ala Val Arg Ile Arg Gly Lys Ser
  1             5

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```

<210> 91
<211> 8
<212> PRT
<213> Unknown

```

```

<220>
<223> Description of Unknown Organism: Consensus P-loop
      Motif Sequence found in large number of protein
      families

```

```

<220>
<221> MOD_RES
<222> (2)..(5)
<223> Wherein Xaa is any residue

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```

<400> 91
Ala Xaa Xaa Xaa Xaa Gly Lys Ser
  1             5

```

```

<210> 92
<211> 17
<212> PRT
<213> Homo sapiens

```

```

<400> 92
Ser Gly Gln Pro Glu Met Glu Pro Pro Arg Arg Pro Ser Gly Cys Val
  1             5             10             15

```

Gly

```

<210> 93
<211> 9
<212> PRT
<213> Unknown

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<220>  
 <223> Description of Unknown Organism: Consensus c-Alb  
 SH3 binding peptide

<220>  
 <221> MOD\_RES  
 <222> (2)..(5)  
 <223> Wherein Xaa is any residue

<220>  
 <221> MOD\_RES  
 <222> (7)..(8)  
 <223> Wherein Xaa is any residue

<400> 93  
 Pro Xaa Xaa Xaa Xaa Pro Xaa Xaa Pro  
           1                          5

<210> 94  
 <211> 17  
 <212> PRT  
 <213> Homo sapiens

<400> 94  
 His Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr  
           1                          5                          10                          15

Pro

<210> 95  
 <211> 14  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Description of Unknown Organism: General Target  
 Sequence Recognized by Hairpin Ribozyme

<220>  
 <221> modified\_base  
 <222> (1)..(3)  
 <223> Wherein N is G, U, C or A

<220>  
 <221> modified\_base  
 <222> (5)  
 <223> Wherein N is G, U, C or A

<220>  
 <221> modified\_base  
 <222> (9)..(14)  
 <223> Wherein N is G, U, C or A

<400> 95  
 nnnbngucnn nnnn 14  
  
 <210> 96  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Amplification  
 Primer Design Based on EST Sequence GenBank  
 Accession Number AA281296  
  
 <400> 96  
 aggagatctc gcgatgccgc gcgctc 26  
  
 <210> 97  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Amplification  
 Primer Design Based on EST Sequence GenBank  
 Accession Number AA281296  
  
 <400> 97  
 tccacgcgctc ctgcccggt g 21  
  
 <210> 98  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Amplification  
 Primer Design Based on EST Sequence GenBank  
 Accession Number AA281296  
  
 <400> 98  
 gctggtgcag cgcggggacc 20  
  
 <210> 99  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Amplification  
 Primer Design Based on EST Sequence GenBank  
 Accession Number AA281296  
  
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 <210> 100  
 <211> 20

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 100  
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<210> 101  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 101  
 cctgcctgaa ggagctggtg 20

<210> 102  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 102  
 ggacacctgg cggaaggag 19

<210> 103  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 103  
 ccgagtgtgtg cagaggctgt 20

<210> 104  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized

Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 104  
gaagccgaag gccagcacgt tctt 24

<210> 105  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 105  
gtgcagctgc tccgccagca ca 22

<210> 106  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 106  
gttcccaagc agtccagaa acag 24

<210> 107  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 107  
ggcagtgctg cttgaggagc a 21

<210> 108  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 108  
cactggctga tgagtgtgta c 21

<210> 109  
 <211> 22  
 <212> DNA  
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<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 109  
 gacgtacaca ctcacagcc ag 22

<210> 110  
 <211> 23  
 <212> DNA  
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<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 110  
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<210> 111  
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<220>  
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 GenBank Accession Number AA281296

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<210> 112  
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<220>  
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 GenBank Accession Number AA281296

<400> 112  
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<210> 113  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 113  
 ttcaccctcg aggtgagacg ct 22

<210> 114  
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 <212> DNA  
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<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 114  
 tcgtagttga gcacgctgaa c 21

<210> 115  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
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 GenBank Accession Number AA281296

<400> 115  
 gcctgagctg tactttgtca a 21

<210> 116  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 116  
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<210> 117  
 <211> 24  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 117  
 gtacatgcga cagttcgtgg ctca 24

<210> 118  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 118  
 catgaagcgt aggaagacgt cgaaga 26

<210> 119  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 119  
 cgcaaacagc ttgttctcca tgtc 24

<210> 120  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthesized  
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 GenBank Accession Number AA281296

<400> 120  
 ctatgcccgg acctccatca ga 22

<210> 121  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 121  
 ctgatggagg tccgggcata g 21

<210> 122

<211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 122  
 cctccgaggc cgtgcagt 18

<210> 123  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 123  
 cacctcaagc tttctagatc agtccaggat ggtcttgaag tca 43

<210> 124  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 124  
 ggaaggcaaa ggagggcagg gcga 24

<210> 125  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 125  
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<210> 126  
 <211> 18  
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<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 126  
gggttgcgga gggtgggc 18

<210> 127  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 127  
gcagtgggtga gccgagtcct g 21

<210> 128  
<211> 20  
<212> DNA  
<213> Artificial Sequence

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Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 128  
cgactttgga ggtgccttca 20

<210> 129  
<211> 20  
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<220>  
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Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 129  
gctggtgcag cgcggggacc 20

<210> 130  
<211> 22  
<212> DNA  
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Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 130

gaggtgcaga gcgactactc ca 22

<210> 131  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 131  
 gtctcacctc gaggtgaag 20

<210> 132  
 <211> 22  
 <212> DNA  
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<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 132  
 ggctgctcct gcgtttggtg ga 22

<210> 133  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 133  
 gccagagatg gagccaccc 19

<210> 134  
 <211> 19  
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<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 134  
 gggtagctcc atctctggc 19

<210> 135  
 <211> 21  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 135

ccgcacgctc atcttccacg t

21

<210> 136

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 136

gcttggggat gaagcggtc

19

<210> 137

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 137

cgcttgagct gtactttgtc a

21

<210> 138

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 138

cacctcaagc tttctagatc agctagcggc ccagcccaac tcccct

46

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence

GenBank Accession Number AA281296

<400> 139  
gcagcacaca tgcgtgaaac ctgt 24

<210> 140  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 140  
gtgtcagaga tgacgcgcag gaa 23

<210> 141  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 141  
acccacactt gcctgtcctg agt 23

<210> 142  
<211> 63  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 142  
actggatcct tgacaattaa tgcacgcgct cgtataatgt gtggagggtt gcggagggtg 60  
ggc 63

<210> 143  
<211> 38  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 143  
ctgtaatacg actcactata gggttgcgga ggggtgggc 38

<210> 144  
 <211> 73  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 144  
 cacctgcaga catgcgtttc gtcctcacgg actcatcagg ccagctggcg acgcatgtgt 60  
 gagccgagtc ctg 73

<210> 145  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 145  
 ggatccgccg cagagcaccg tctg 24

<210> 146  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 146  
 cgaagctttc agtgggccgg catctgaac 29

<210> 147  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthesized  
 Amplification Primer Design based on EST Sequence  
 GenBank Accession Number AA281296

<400> 147  
 cgaagctttc acaggcccag cccaactcc 29

<210> 148  
 <211> 26  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 148

gcggatccag agccacgtcc tacgtc

26

<210> 149

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthesized  
Amplification Primer Design based on EST Sequence  
GenBank Accession Number AA281296

<400> 149

gcggatccgt tcagatgccg gcccac

26

<210> 150

<211> 9

<212> PRT

<213> Homo sapiens

<400> 150

Pro Glu Met Glu Pro Pro Arg Arg Pro  
1 5

<210> 151

<211> 4

<212> PRT

<213> Homo sapiens

<400> 151

Ala Ala Glu His  
1

<210> 152

<211> 6

<212> PRT

<213> Homo sapiens

<400> 152

Val Gln Met Pro Ala His  
1 5

<210> 153

<211> 5

<212> PRT

<213> Homo sapiens

<400> 153  
Val Gly Leu Gly Leu  
1 5

<210> 154  
<211> 4  
<212> PRT  
<213> Homo sapiens

<400> 154  
Arg Ala Thr Ser  
1

<210> 155  
<211> 622  
<212> PRT  
<213> Homo sapiens

<220>  
<223> N-Terminal Truncated Telomerase (ver.2); encoded  
by SEQ ID NO:51, with Y Intron ORF3

<400> 155  
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser  
1 5 10 15  
His Thr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly  
20 25 30  
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg  
35 40 45  
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro  
50 55 60  
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Pro Pro Arg Gly Arg Arg  
65 70 75 80  
Pro Ala Gly Val Glu Gly Gly Arg Gly Glu Pro Ala Thr Cys Gly Glu  
85 90 95  
Gln Arg Arg Arg Leu Arg Ala Leu Pro Pro Gln Val Ser Cys Leu Lys  
100 105 110  
Glu Leu Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys  
115 120 125  
Asn Val Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly  
130 135 140  
Pro Pro Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr  
145 150 155 160  
Val Thr Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg

✓

465                      470                      475                      480  
 Arg Leu Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr  
                                  485                      490                      495  
 Gly Phe Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp  
                                  500                      505                      510  
 Gly Ser Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe  
                                  515                      520                      525  
 Ile Ser Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp  
                                  530                      535                      540  
 Lys Met Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val  
                                  545                      550                      555                      560  
 Gly Cys Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala  
                                  565                      570                      575  
 Lys Phe Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg  
                                  580                      585                      590  
 Ser Phe Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe  
                                  595                      600                      605  
 Phe Tyr Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly  
                                  610                      615                      620

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